

## Table 1 - T34E200T

6800 chip human RA PBMC

name	qualifier	GenoSpring qualifier	Patients called "p">4	#"p" (RA)	Avg Freq RA	Patients called "p">4	#"p" Normals	#"p" (Normal)	Avg Freq Normals	Ratio	Fold Change	Symbol	Chromosome	Description	function
MR110000	D64154 at	D64154	fail	4		PASS	13	4	9.77	Normal	Normal	RAC2	22q12-q13.2	Mr 110,000 antigen	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)
RAC2	M64595 at	M64595	fail	3		PASS	13	3	19.85	Normal	Normal			ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	membrane glycoprotein
J03263 s at	J03263 s at	J03263	fail	3		PASS	13	3	9.23	Normal	Normal	LAMP1		thromboxane A synthase 1 (platelet, cytochrome P450, subfamily V)	thromboxane A synthase 1 (platelet, cytochrome P450, subfamily V)
TBXAS1	M80647 at	M80647	fail	4		PASS	12	4	17.42	Normal	Normal	TBXAS1	7q34-q35	thromboxane A synthase 1 (platelet, cytochrome P450, subfamily V)	thromboxane A synthase 1 (platelet, cytochrome P450, subfamily V)
ALDR1	J04794 at	J04794	fail	4		PASS	12	4	14.42	Normal	Normal	ALDR1		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	aldehyde reductase (EC 1.1.1.2)
HADHA	D16480 at	D16480	fail	2		PASS	12	2	16.33	Normal	Normal	HADHA	2p23	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit
M13929 s at	M13929 s at	M13929	fail	1		PASS	12	1	9.33	Normal	Normal	MYC		c-myc-P64 protein	ORF 114; putative similar to mouse LysF-1, encoded by GenBank Accession Number S74708; similar to mouse Ikars DNA-binding protein, Swiss-Prot Accession Number Q03267
HLK1	U40462 at	U40462	fail	1		PASS	12	1	6.42	Normal	Normal	hlk-1		Ikars/Lyf-1 homolog	mannosidase, alpha type II
MANA2	D63998 at	D63998	fail	1		PASS	12	1	5.25	Normal	Normal	MANA2	5	mannosidase, alpha type II	mannosidase, alpha type II
ITBA2	X92896 at	X92896	fail	0		PASS	12	0	6.42	Normal	Normal	ITBA2		protein phosphatase inhibitor 2	
PPP1R2	U68111 at	U68111	fail	0		PASS	12	0	5.17	Normal	Normal	PPP1R2		FYN-binding protein (FYN-120/130)	FYN-binding protein (FYN-120/130)
LCP2	U93049 at	U93049	fail	3		PASS	11	3	11.82	Normal	Normal	FYB		protein phosphatase inhibitor 2	
PCNA	J05614 at	J05614	fail	3		PASS	11	3	11.73	Normal	Normal			RNA polymerase II	
POLR2B	L37127 at	L37127	fail	2		PASS	11	2	13.27	Normal	Normal			rab8 small GTP binding	
DG	HG1872-HT	HG1872-HT	fail	2		PASS	11	2	10.55	Normal	Normal			dihydropyrimidine dehydrogenase	
MEL	X56741 at	X56741	fail	2		PASS	11	2	7.82	Normal	Normal	rab8		dihydropyrimidine dehydrogenase	
U09178 s at	U09178 s at	U09178	fail	2		PASS	11	2	6.91	Normal	Normal	DPYD	1p22	CALM	
CALM	U45976 at	U45976	fail	2		PASS	11	2	6.91	Normal	Normal	CALM		transducin-like enhancer of split 4, homolog of Drosophila E(gp1)	transducin-like enhancer of split 4, homolog of Drosophila E(gp1)
TLE4	M99439 at	M99439	fail	2		PASS	11	2	5.73	Normal	Normal	TLE4		heat shock 70kD protein 4	heat shock 70kD protein 4
HSPA4	L12723 at	L12723	fail	2		PASS	11	2	5.45	Normal	Normal	HSPA4	5q31.1-q31.2	nuclear protein p40	cell proliferation-associated protein
NUCP40	U86602 at	U86602	fail	2		PASS	11	2	5.09	Normal	Normal			T-complex protein 1, Beta subunit (TCP-1-BETA)	
E_CIT987SK	U91327 at	U91327	fail	1		PASS	11	1	5.82	Normal	Normal	99D8.1		FKBP-rapamycin associated protein	FK-506 binding protein 12-rapamycin associated protein 1
FRAP	L34075 at	L34075	fail	1		PASS	11	1	5.73	Normal	Normal	FRAP1	1p36.2	eukaryotic translation initiation factor 2, subunit 3 (gamma, 52kD)	eukaryotic translation initiation factor 2, subunit 3 (gamma, 52kD)
EIF2G	L19161 at	L19161	fail	1		PASS	11	1	5.64	Normal	Normal	EIF2G3	Xp22.2-p22.1	E46-like contains exons 2-9 continues in 284478	E46-like contains exons 2-9 continues in 284478
P_E46	Z93784 at	Z93784	fail	1		PASS	11	1	5.36	Normal	Normal	U398C22.1		ubiquitin carboxyl-terminal hydrolase	ubiquitin carboxyl-terminal hydrolase
UCHL3	M30496 at	M30496	fail	1		PASS	11	1	4.27	Normal	Normal				

RPAL	M63488_at	M63488	fail	0	PASS	11	0	7.45	Normal	Normal	RPAL	17	replication protein A1 (70kD)	replication protein A1 (70kD)
RINF	HG511-HT5	HG511-HT5	fail	0	PASS	11	0	5.36	Normal	Normal				
M26041_s_a	M26041_s_a	M26041	fail	3	PASS	10	3	20.70	Normal	Normal	HLA-DQA1	6p21.3	major histocompatibility complex, class II, DQ alpha 1	major histocompatibility complex, class II, DQ alpha 1
K91_PCSK	D42053_at	D42053	fail	2	PASS	10	2	6.70	Normal	Normal	SIP	16	site-1 protease (ubiquitin-like, sterol-regulated, cleaves sterol regulatory element binding proteins)	site-1 protease (ubiquitin-like, sterol-regulated, cleaves sterol regulatory element binding proteins)
KCNQ1	U40990_at	U40990	fail	2	PASS	10	2	6.70	Normal	Normal	KVLQT1		voltage gated potassium channel, KVLQT1 (Krabbe disease)	galactosylceramidase (Krabbe disease)
GALC	L23116_at	L23116	fail	2	PASS	10	2	5.40	Normal	Normal	GALC	14q31	galactosylceramidase (Krabbe disease)	galactosylceramidase (Krabbe disease)
KPNB3	U72761_at	U72761	fail	2	PASS	10	2	5.40	Normal	Normal	KPNB3		karyopherin (importin) beta 3	karyopherin (importin) beta 3
DR1	M97388_at	M97388	fail	2	PASS	10	2	5.30	Normal	Normal	DR1	1p22.1	down-regulator of transcription 1, TBP-binding (negative cofactor 2)	down-regulator of transcription 1, TBP-binding (negative cofactor 2)
RFC4	M87339_at	M87339	fail	2	PASS	10	2	5.20	Normal	Normal	RFC4	3q27	replication factor C (activator 1) 4	replication factor C (activator 1) 4
BIOBM	APFX-BioB	APFX-BioB	fail	1	PASS	10	1	7.20	Normal	Normal				
UBE2D1	HG33444-HT	HG33444-HT	fail	1	PASS	10	1	6.50	Normal	Normal				
MANA2	L28821_at	L28821	fail	1	PASS	10	1	6.30	Normal	Normal	MANA2	15q25	alpha mannosidase II isozyme	mannosidase, alpha, class 2A, member 2
CAMK2A	U81554_at	U81554	fail	1	PASS	10	1	5.50	Normal	Normal	CAMK2G	10q22	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma
HG2797-HT2	HG2797-HT2	HG2797-HT2	fail	1	PASS	10	1	5.20	Normal	Normal				
POH1	U86782_at	U86782	fail	1	PASS	10	1	5.00	Normal	Normal	POH1		26S proteasome-associated pad1 homolog	human homolog of fission yeast pad1
GZMM	HG3104-HT	HG3104-HT	fail	0	PASS	10	0	16.20	Normal	Normal				
BAP	U72512_at	U72512	fail	3	PASS	9	3	13.56	Normal	Normal				
ESD	D28416_at	D28416	fail	3	PASS	9	3	10.89	Normal	Normal				
KO1160_s_at	KO1160_s_at	KO1160	fail	3	PASS	9	3	9.22	Normal	Normal				
U45878_s_at	U45878_s_at	U45878	fail	3	PASS	9	3	10.00	Normal	Normal				
RPS4Y	M38459_at	M38459	fail	2	PASS	9	2	44.67	Normal	Normal	RPS4Y	Yp1.3	inhibitor of apoptosis protein 1	HIAP-1
LTR	M92449_at	M92449	fail	2	PASS	9	2	9.89	Normal	Normal	PLT		ribosomal protein S4, Y-linked	ribosomal protein S4, Y-linked
FBP1	U05040_at	U05040	fail	2	PASS	9	2	7.67	Normal	Normal	FUBP		FUSE-binding protein	putative far upstream element binding protein
CD27	M63928_at	M63928	fail	2	PASS	9	2	7.44	Normal	Normal	TNFRSF7	12p13	CD27 antigen	tumor necrosis factor receptor superfamily, member 7
FGFR1	U28811_at	U28811	fail	2	PASS	9	2	6.11	Normal	Normal	CFR-1		cysteine-rich fibroblast growth factor receptor	
PTPRA	M34668_at	M34668	fail	2	PASS	9	2	5.67	Normal	Normal	PTPRA	20p13	protein tyrosine phosphatase, receptor type, alpha	protein tyrosine phosphatase, receptor type, alpha polypeptide
U52191_s_at	U52191_s_at	U52191	fail	2	PASS	9	2	5.56	Normal	Normal	SMCY	Yq	SMC (mouse) homolog, Y chromosome	SMC (mouse) homolog, Y chromosome
U72935_cds	U72935_cds	U72935	fail	2	PASS	9	2	5.22	Normal	Normal	ATRX		putative DNA dependent ATPase and helicase	XH2; XNP; alternately spliced product 1; translation starts in exon 9
CBR	J04056_at	J04056	fail	2	PASS	9	2	4.89	Normal	Normal	CBR1	21q22.1	carboxyl reductase 1	carboxyl reductase 1
HSPB1	Z23090_at	Z23090	fail	1	PASS	9	1	12.56	Normal	Normal	HSPB1	7q	heat shock 27kD protein 1	heat shock 27kD protein 1
STAT1mb	APFX-HUM	APFX-HUM	fail	1	PASS	9	1	7.00	Normal	Normal				
K129_RPPT	D50919_at	D50919	fail	1	PASS	9	1	4.89	Normal	Normal	KIAA0129		KIAA0129 gene product	KIAA0129 gene product

CDK7	L20320_at	L20320	fail	1	PASS	9	1	4.89	Normal	Normal	CDK7	2p15-cen	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)
FABP5	M94856_at	M94856	fail	1	PASS	9	1	4.78	Normal	Normal	FABP5		fatty acid binding protein 5 (psoriasis-associated)	fatty acid binding protein 5 (psoriasis-associated)
ICSBP1	M91196_at	M91196	fail	0	PASS	9	0	8.33	Normal	Normal	ICSBP1		interferon consensus sequence binding protein 1	interferon consensus sequence binding protein 1
NMT1	M86707_at	M86707	fail	0	PASS	9	0	7.33	Normal	Normal	NMT1		N-myristoyltransferase 1	N-myristoyltransferase 1
RAB4	M28211_at	M28211	fail	0	PASS	9	0	5.11	Normal	Normal	RAB4	1q42-q43	RAB4, member RAS oncogene family	RAB4, member RAS oncogene family
ERPRT	M27826_at	M27826	fail	2	PASS	8	2	10.63	Normal	Normal			neutral protease large subunit	
EV12A	M55267_at	M55267	fail	2	PASS	8	2	10.13	Normal	Normal	EV12A		EV12 protein	
H2BH_f	Z80780_f	Z80780	fail	1	PASS	8	1	9.88	Normal	Normal	H2BH		histone H2B	
TIP60	U74667_at	U74667	fail	0	PASS	8	0	7.25	Normal	Normal	TIP60		histone H2B	interacts with HIV1 Tat; similar to acetyltransferase; similar to yeast SAS2, SAS3 and human MOZ, encoded by GenBank Accession Numbers U14548, Z23261 and U47742, respectively; similar to sequence with GenBank Accession Number U40989
PHB	S85655_at	S85655	fail	0	PASS	8	0	6.63	Normal	Normal	PHB	17q21	prohibitin	prohibitin
EPHB4	U07695_at	U07695	fail	0	PASS	8	0	6.50	Normal	Normal	EPHB4	7	EPHB4	EPHB4
SNAP23	U55936_at	U55936	fail	0	PASS	8	0	6.00	Normal	Normal	SNAP23		synaptoosomal-associated protein, 23kD	synaptoosomal-associated protein, 23kD
D26155_s_at	D26155_s_at	D26155	fail	0	PASS	8	0	5.13	Normal	Normal	SMARCA2	9p24-p23	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2
PRP4H	U48736_at	U48736	fail	0	PASS	8	0	5.00	Normal	Normal	PRP4		serine/threonine-protein kinase PRP4 homolog	serine/threonine-protein kinase PRP4 homolog
IL16	HG270-HT2	HG270-HT2	fail	0	PASS	8	0	4.75	Normal	Normal				
E_E18CPGE	HG3991-HT2	HG3991-HT2	fail	4	PASS	7	4	30.57	Normal	Normal				
RORET	U90547_at	U90547	fail	4	PASS	7	4	12.14	Normal	Normal	RoRet		Ro/SSA ribonucleoprotein homolog	Ro/SSA ribonucleoprotein homolog
HMG1Y_ma	L17131_ma	L17131	fail	4	PASS	7	4	9.71	Normal	Normal	HMG1Y	6p	high-mobility group (nonhistone chromosomal) protein isoforms I and Y	high-mobility group (nonhistone chromosomal) protein isoforms I and Y
AFFX-BioDn	AFFX-BioDn	AFFX-BioDn	fail	2	PASS	7	2	12.29	Normal	Normal				
TXBP181	U33822_at	U33822	fail	1	PASS	7	1	9.86	Normal	Normal	MAD1L1	7p22	MAD1 (mitotic arrest deficient, yeast, homolog)-like 1	MAD1 (mitotic arrest deficient, yeast, homolog)-like 1
NUCB	U31342_at	U31342	fail	0	PASS	7	0	6.14	Normal	Normal				
DPH2L	U34880_at	U34880	fail	0	PASS	7	0	6.00	Normal	Normal	DPH2L1	17p13.3	diphtheria toxin resistance protein required for diphtheria toxin resistance	diphtheria toxin resistance protein required for diphtheria toxin resistance
TRAP1	U12595_at	U12595	fail	0	PASS	7	0	5.71	Normal	Normal	TRAP1		tumor necrosis factor type 1 receptor associated protein	TNF type 1 receptor associated protein
X60003_s_at	X60003_s_at	X60003	fail	0	PASS	7	0	5.43	Normal	Normal	delta CREB			
20GCP_ma	X66114_ma	X66114	fail	0	PASS	7	0	5.43	Normal	Normal	SLC20A4	17p13.3	solute carrier family 20 (oxoglutarate carrier), member 4	solute carrier family 20 (oxoglutarate carrier), member 4
K196	D83780_at	D83780	fail	0	PASS	7	0	5.14	Normal	Normal	KIAA0196		KIAA0196 gene product	KIAA0196 gene product

K52_SK12P	D29641_at	D29641	fail	0		PASS	7	0	5.00	Normal	Normal	KIAA0052				
CUL4A	U58090_at	U58090	fail	0		PASS	7	0	5.00	Normal	Normal	CUL4A		Hs-CUL-4A		cullin 4A
E_23707	U79270_at	U79270	fail	0		PASS	7	0	5.00	Normal	Normal	COX11	17q22	cytochrome c oxidase subunit 11		cytochrome c oxidase subunit 11
BLK	S76617_at	S76617	fail	0		PASS	7	0	4.71	Normal	Normal	BLK	8p23-p22	B lymphoid tyrosine kinase		B lymphoid tyrosine kinase
U69140_s_at	U69140_s_at	U69140	fail	0		PASS	7	0	4.71	Normal	Normal			syndapin interacting protein; Human ortholog of rat zyginn1		syndapin interacting protein; Human ortholog of rat zyginn1
ERPL1	X89211_at	X89211	fail	0		PASS	7	0	4.71	Normal	Normal	HERV-L		Human Endogenous Retrovirus-Like elements (HERV-L)/pseudogene		Human Endogenous Retrovirus-Like elements (HERV-L)/pseudogene
PRTKI	S76965_at	S76965	fail	0		PASS	7	0	4.57	Normal	Normal			protein kinase inhibitor, PKI		This sequence comes from Fig.1B; PKI
X93511_s_at	X93511_s_at	X93511	fail	0		PASS	7	0	4.00	Normal	Normal	orf1		telomeric DNA binding protein		telomeric DNA binding protein
MAGEP15	U19796_at	U19796	fail	7	23.29	fail	3	7		Disease	Disease			melanoma antigen p15		melanoma antigen p15
HG3148-HT	HG3148-HT	HG3148-HT	PASS	7	12.86	fail	3	7		Disease	Disease			metastasis associated 1		metastasis associated 1
MTA1	U35113_at	U35113	PASS	7	6.71	fail	1	7		Disease	Disease	MTA1		metastasis associated 1		metastasis associated 1
HG4120-HT	HG4120-HT	HG4120-HT	PASS	6	5.17	fail	3	6		Disease	Disease			metastasis associated 1		metastasis associated 1
AVPR1B	L37112_at	L37112	PASS	6	15.00	fail	3	6		Disease	Disease			metastasis associated 1		metastasis associated 1
ACRV1_ma	S65583_ma	S65583	PASS	6	12.83	fail	3	6		Disease	Disease	SP-10		metastasis associated 1		metastasis associated 1
U57623_s_at	U57623_s_at	U57623	PASS	6	6.33	fail	3	6		Disease	Disease			metastasis associated 1		metastasis associated 1
AACT_ma	X68733_ma	X68733	PASS	6	10.50	fail	3	6		Disease	Disease	ACT		metastasis associated 1		metastasis associated 1
D29675_s_at	D29675_s_at	D29675	PASS	6	16.50	fail	2	6		Disease	Disease	KCNMA1	10	metastasis associated 1		metastasis associated 1
SLO	U02632_at	U02632	PASS	6	5.67	fail	2	6		Disease	Disease			metastasis associated 1		metastasis associated 1
MME	J03779_at	J03779	PASS	6	28.50	fail	1	6		Disease	Disease	MME	3q21-q27	metastasis associated 1		metastasis associated 1
K246 NOTC	D87433_at	D87433	PASS	6	38.33	fail	1	6		Disease	Disease	KIAA0246		metastasis associated 1		metastasis associated 1
MDC	U83171_at	U83171	PASS	6	14.00	fail	0	6		Disease	Disease	SCYA22	16q13	metastasis associated 1		metastasis associated 1
M22403_s_at	M22403_s_at	M22403	PASS	5	6.40	fail	1	5		Disease	Disease	GP1BA	17pter-p12	metastasis associated 1		metastasis associated 1
FSTRP	U06863_at	U06863	PASS	5	8.80	fail	1	5		Disease	Disease			metastasis associated 1		metastasis associated 1
PLCG2H	U45974_at	U45974	PASS	5	15.40	fail	0	5		Disease	Disease			metastasis associated 1		metastasis associated 1
PTPRN	L18983_at	L18983	PASS	5	20.00	fail	0	5		Disease	Disease	PTPRN	2q35-q36.1	metastasis associated 1		metastasis associated 1
AQP9	AB006190_a	AB006190	PASS	5	10.20	fail	0	5		Disease	Disease	AQP7	9p13	metastasis associated 1		metastasis associated 1





# FOREFOREWORD

J03260_s_at	J03260_s_at	J03260	PASS	7	28.71	PASS	7	8.57	3.35	3.35	GNAZ	22q11.1-q11.2	guanine nucleotide binding protein (G protein), alpha 2 polypeptide	guanine nucleotide binding protein (G protein), alpha 2 polypeptide
CDC25	S78187_at	S78187	PASS	9	63.89	PASS	13	19.08	3.35	3.35	CDC25B	20p13	cell division cycle 25B	cell division cycle 25B
RELA	L19067_at	L19067	PASS	9	39.78	PASS	10	11.90	3.34	3.34			NF-kappa-B transcription factor subunit	putative
XQTP	D16469_at	D16469	PASS	9	31.67	PASS	11	9.55	3.32	3.32	ATP6S1	Xq28	ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1	ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1
RAGE_cds1	U89136_cds	U89136	PASS	9	71.78	PASS	13	21.69	3.31	3.31	HBX2		homeobox PBX2 gene	by a contig of ESTs with GenBank Accession Numbers W76064, R59617, W72507
K154_ADTC	D63876_at	D63876	PASS	9	33.89	PASS	12	10.25	3.31	3.31	KIAA0154		KIAA0154 gene product is related to mouse gamma adaptin.	KIAA0154 gene product is related to mouse gamma adaptin.
PRSM1	U58048_at	U58048	PASS	8	18.63	PASS	9	5.67	3.29	3.29	PRSM1	16q24.3	protease, metallo, 1, 33kD	protease, metallo, 1, 33kD
ATP6C	M62762_at	M62762	PASS	9	69.67	PASS	13	21.23	3.28	3.28	ATP6C	16p13.3	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD
NCF1	M55067_at	M55067	PASS	9	72.33	PASS	13	22.08	3.28	3.28	NCF1	7q11.23	neutrophil cytosolic factor 1	neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1)
K220	D86974_at	D86974	PASS	9	239.22	PASS	13	73.38	3.26	3.26	KIAA0220			
K109_CLAS	D63475_at	D63475	PASS	8	45.88	PASS	13	14.15	3.24	3.24	CLAPM1	3q28	clathrin-associated/assembly/adaptor protein, medium 1	clathrin-associated/assembly/adaptor protein, medium 1
TSC2	L48546_at	L48546	PASS	9	30.44	PASS	7	9.43	3.23	3.23	TSC2	16p13.3	tuberous sclerosis 2	tuberous sclerosis 2
EDR2	U89278_at	U89278	PASS	8	25.25	PASS	12	7.83	3.22	3.22	EDR2		early development regulator 2 (homolog of polyhomeotic 2)	early development regulator 2 (homolog of polyhomeotic 2)
M34996_s_a	M34996_s_a	M34996	PASS	9	80.56	PASS	13	25.08	3.21	3.21	PNUTL1	22q11.2	peanut (Drosophila)-like 1	peanut (Drosophila)-like 1
U59632_s_at	U59632_s_at	U59632	PASS	9	97.22	PASS	13	30.54	3.18	3.18	USP11	Xp21.2-p11.2	Ubiquitin carboxyl-terminal hydrolase, X-linked	ubiquitin specific protease 11
UHX1	U44839_at	U44839	PASS	9	60.22	PASS	13	18.92	3.18	3.18			uroporphyrinogen decarboxylase	
UROD	X89267_at	X89267	PASS	5	47.60	PASS	8	15.25	3.12	3.12			phospholipase C, beta 2	phospholipase C, beta 2
PLCB2	M95678_at	M95678	PASS	9	84.00	PASS	12	26.92	3.12	3.12	PLCB2	15q15	bone marrow stromal cell antigen 2	bone marrow stromal cell antigen 2
BST2	D28137_at	D28137	PASS	8	51.13	PASS	13	16.38	3.12	3.12	BST2	19p13.2	nuclear factor erythroid 2 isoform f, transcription factor	nuclear factor erythroid 2 isoform f, transcription factor
NFER2	S77763_at	S77763	PASS	9	32.33	PASS	11	10.36	3.12	3.12			basic leucine zipper protein; This sequence comes from Fig. 1; transcription factor (NF-E2)	basic leucine zipper protein; This sequence comes from Fig. 1; transcription factor (NF-E2)
EBV1P	U19261_at	U19261	PASS	6	22.67	PASS	7	7.29	3.11	3.11			Epstein-Barr virus-induced protein	EBV induced protein
28SRNAM	AFFX-M278	AFFX-M278	PASS	5	91.00	PASS	7	29.29	3.11	3.11			glutathione S-transferase Zeta 1	glutathione S-transferase Zeta 1
GSTZ1	U86529_at	U86529	PASS	9	25.56	PASS	11	8.27	3.09	3.09	GSTZ1	14q24.3	CD151 antigen	CD151 antigen
CD151	D29963_at	D29963	PASS	8	31.13	PASS	7	10.14	3.07	3.07	CD151	11p15.5	spermidine/spermine N1-acetyltransferase	spermidine/spermine N1-acetyltransferase
SAT_mal	U40369_mal	U40369	PASS	9	37.67	PASS	13	12.31	3.06	3.06	SAT	Xp22.1		

# FOFET " FGF200T"

CLU	M63379_at	M63379	PASS	9	222.78	PASS	13	9	72.85	3.06	3.06	CLU	8p21-p12	clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)	clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)
HMG1	D63874_at	D63874	PASS	9	83.22	PASS	13	9	27.31	3.05	3.05	HMG1	13q12	high-mobility group (nonhistone chromosomal) protein 1	high-mobility group (nonhistone chromosomal) protein 1
DEFA1	M26602_at	M26602	PASS	7	185.43	PASS	11	7	61.09	3.04	3.04	DEFA1	8p23.2-p23.1	defensin, alpha 1, myeloid-related sequence	defensin, alpha 1, myeloid-related sequence
FCGR1A	J04162_at	J04162	PASS	9	46.56	PASS	13	9	15.38	3.03	3.03	FCGR3A	1q23	FC fragment of IgG, low affinity IIIa, receptor for (CD16)	FC fragment of IgG, low affinity IIIa, receptor for (CD16)
M32304_s_a	M32304_s_a	M32304	PASS	8	26.75	PASS	13	8	8.85	3.02	3.02	TIMP2	17q25	tissue inhibitor of metalloproteinase 2	tissue inhibitor of metalloproteinase 2
LSP1	M33552_at	M33552	PASS	9	48.11	PASS	13	9	15.92	3.02	3.02	LSP1		lymphocyte-specific protein 1 (LSP1)	lymphocyte-specific protein 1 (LSP1)
U83239_s_at	U83239_s_at	U83239	PASS	6	34.33	PASS	11	6	11.36	3.02	3.02			CC chemokine STCP-1	CC chemokine STCP-1
GSTH	U90313_at	U90313	PASS	9	43.22	PASS	13	9	14.31	3.02	3.02	GSTTLP28		glutathione-S-transferase like	glutathione-S-transferase like
IL1T1	U82275_at	U82275	PASS	8	27.88	PASS	12	8	9.25	3.01	3.01			immunoglobulin-like transcript 1	immunoglobulin-like transcript 1
NRGN_ma1	X99076_ma1	X99076	PASS	9	230.11	PASS	13	9	76.54	3.01	3.01	NRGN		neurogranin	neurogranin
UBA52	M26880_at	M26880	PASS	9	198.00	PASS	13	9	66.31	2.99	2.99	UBA52	19p13.1-p12	ubiquitin A-52 residue ribosomal protein fusion product 1	ubiquitin A-52 residue ribosomal protein fusion product 1
TMEM1	D26579_at	D26579	PASS	9	31.56	PASS	13	9	10.62	2.97	2.97	ADAM8	10q26.3	a disintegrin and metalloprotease domain 8	a disintegrin and metalloprotease domain 8
GPI	K03515_at	K03515	PASS	9	35.78	PASS	13	9	12.08	2.96	2.96	GPI	19q13.1	glucose phosphate isomerase	glucose phosphate isomerase
TYL	X99688_at	X99688	PASS	9	23.44	PASS	12	9	7.92	2.96	2.96	TYL		ubiquitin-activating enzyme E1 like	ubiquitin-activating enzyme E1 like
UBE1L	L13852_at	L13852	PASS	9	54.78	PASS	13	9	18.62	2.94	2.94	UBE1L	3p21	ubiquitin-activating enzyme E1 like	ubiquitin-activating enzyme E1 like
KRT1_ma1	M98776_ma1	M98776	PASS	7	19.29	PASS	9	7	6.56	2.94	2.94	KRT1		keratin 1	keratin 1
K45_YKL	D28476_at	D28476	PASS	9	27.44	PASS	12	9	9.33	2.94	2.94	TRIP12		thyroid hormone receptor interactor 12	thyroid hormone receptor interactor 12
HCFC1	L20010_at	L20010	PASS	8	26.13	PASS	13	8	8.92	2.93	2.93	SLC9A1	1p36.1-p35	Na+/H+ exchanger NHE-1 isoform	Na+/H+ exchanger NHE-1 isoform
SLC9A1	S68616_at	S68616	PASS	5	20.20	PASS	10	5	6.90	2.93	2.93	SLC9A1		solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (anion, Na+/H+, amiloride sensitive)	solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (anion, Na+/H+, amiloride sensitive)
SCYA5	M21121_at	M21121	PASS	9	156.78	PASS	13	9	53.69	2.92	2.92	SCYA5	17q11.2-q12	small inducible cytokine A5 (RANTES)	small inducible cytokine A5 (RANTES)
PRKMK3	D87116_at	D87116	PASS	9	32.89	PASS	11	9	11.27	2.92	2.92	PRKMK3	17q11.2	protein kinase, mitogen-activated, kinase 3 (MAP kinase kinase 3)	protein kinase, mitogen-activated, kinase 3 (MAP kinase kinase 3)
CCND3	M9287_at	M9287	PASS	9	68.33	PASS	13	9	23.62	2.89	2.89	CCND3	6p21	cyclin D3	cyclin D3
SMN1_ma2	U80017_ma2	U80017	PASS	8	18.38	PASS	11	8	6.36	2.89	2.89	bt2p44		basic transcription factor 2 p44	basic transcription factor 2 p44
PLCG2H	U45975_at	U45975	PASS	6	23.50	PASS	7	6	8.14	2.89	2.89			phosphatidylinositol (4,5)bisphosphate 5-phosphatase homolog	phosphatidylinositol (4,5)bisphosphate 5-phosphatase homolog
X74874_ma1	X74874_ma1	X74874	PASS	8	19.75	PASS	13	8	6.85	2.88	2.88			RNA polymerase II largest subunit	RNA polymerase II largest subunit
M36118_s_a	M36118_s_a	M36118	PASS	8	33.63	PASS	12	8	11.67	2.88	2.88	GZMB	14q11.2	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)

# Table 206

IMPDH1	J05272_at	J05272	PASS	9	31.44	PASS	13	9	10.92	2.88	2.88	IMPDH1	7q31.3-q32	IMP (inosine monophosphate) dehydrogenase 1	IMP (inosine monophosphate) dehydrogenase 1
S40719 s at	S40719 s at	S40719	PASS	9	19.89	PASS	11	9	6.91	2.88	2.88	GFAP	17q21	glial fibrillary acidic protein	glial fibrillary acidic protein
NAP1L4	U77456 at	U77456	PASS	6	29.50	PASS	12	6	10.25	2.88	2.88			nucleosome assembly protein 2	nucleosome assembly protein 2
E ZNF162	L49380 at	L49380	PASS	9	46.44	PASS	13	9	16.15	2.88	2.88	ZNF162	11q13	zinc finger protein 162	zinc finger protein 162
SI00A12	D83657_at	D83657	PASS	9	65.44	PASS	13	9	22.77	2.87	2.87			CAAF1 (calcium-binding protein in amniotic fluid 1)	CAAF1 (calcium-binding protein in amniotic fluid 1)
K56	D29954 at	D29954	PASS	8	18.88	PASS	7	8	6.57	2.87	2.87	KIAA0056		CHL1 protein	CHL1 protein
E DDX11	U75968 at	U75968	PASS	9	20.56	PASS	12	9	7.17	2.87	2.87	CHLR1		150 kDa oxygen-regulated protein ORP150	150 kDa oxygen-regulated protein ORP150
ORP150	U65785_at	U65785	PASS	9	33.67	PASS	12	9	11.75	2.87	2.87			ADP-ribosylation factor 5	ADP-ribosylation factor 5
ARF5	M57567 at	M57567	PASS	8	46.00	PASS	13	8	16.15	2.85	2.85	ARF5	7q31.3	protease inhibitor 6 (placental thrombin inhibitor)	protease inhibitor 6 (placental thrombin inhibitor)
S69272_s at	S69272_s at	S69272	PASS	9	24.67	PASS	13	9	8.69	2.84	2.84	P16	6p25	MAP-kinase activating death domain	MAP-kinase activating death domain
AB002356_s	AB002356_s	AB002356	PASS	9	31.67	PASS	12	9	11.17	2.84	2.84	MADD	11p11.21-p11.22	regulator of G-protein signalling 2, 24kD	regulator of G-protein signalling 2, 24kD
CSF1	HG1155-HT4	HG1155-HT4	PASS	8	27.63	PASS	9	8	9.78	2.83	2.83	RGS2	1q31	uridine phosphorylase	uridine phosphorylase
RGS2	L13391_at	L13391	PASS	9	60.33	PASS	13	9	21.38	2.82	2.82			2',3'-cyclic-nucleotide 3'-phosphodiesterase (CNP1)	KIAA0250 gene product alternative splicing
UP	X90858 at	X90858	PASS	9	21.44	PASS	13	9	7.62	2.82	2.82	UP	7	cytidine deaminase	cytidine deaminase
K250	D87437 at	D87437	PASS	9	19.33	PASS	9	9	6.89	2.81	2.81	KIAA0250		FAST kinase	FAST kinase
CNP_cds1	D13146_cds1	D13146	PASS	9	49.89	PASS	13	9	17.85	2.80	2.80			c-src tyrosine kinase	c-src tyrosine kinase
CDA	L27943 at	L27943	PASS	6	32.33	PASS	10	6	11.60	2.79	2.79	CDA	1p36.2-p35	D component of complement (adipsin)	D component of complement (adipsin)
FAST	X86779 at	X86779	PASS	9	20.33	PASS	10	9	7.30	2.79	2.79	fast		hepatitis C-associated microtubular aggregate protein p44	hepatitis C-associated microtubular aggregate protein p44
X59932_s at	X59932_s at	X59932	PASS	9	62.44	PASS	13	9	22.46	2.78	2.78	CSK	15q23-q25	CD33 antigen (gp67)	CD33 antigen (gp67)
MAZ	M94046 at	M94046	PASS	9	29.67	PASS	13	9	10.69	2.77	2.77			14-3-3 protein eta chain	14-3-3 protein eta chain
DF	M84526 at	M84526	PASS	5	43.40	PASS	12	5	15.67	2.77	2.77	DF		clathrin, light polypeptide (Lea)	clathrin, light polypeptide (Lea)
PRKM3	D28915_at	D28915	PASS	7	16.00	PASS	10	7	5.80	2.76	2.76			myeloid cell leukemia sequence 1 (BCL2-related)	myeloid cell leukemia sequence 1 (BCL2-related)
CD33	M23197 at	M23197	PASS	8	21.00	PASS	13	8	7.62	2.76	2.76	CD33	19q13.3	tumor necrosis factor receptor superfamily, member 1B	tumor necrosis factor receptor superfamily, member 1B
D78577 s at	D78577 s at	D78577	PASS	9	85.67	PASS	13	9	31.08	2.76	2.76			guanine nucleotide binding protein 10	guanine nucleotide binding protein 10
BRF2	X78992 at	X78992	PASS	8	64.88	PASS	13	8	23.54	2.76	2.76	ERF-2		polymerase (RNA) II (DNA directed) polypeptide E (25kD)	polymerase (RNA) II (DNA directed) polypeptide E (25kD)
CLTA	M20471 at	M20471	PASS	9	73.56	PASS	12	7	6.75	2.75	2.75	CLTA	12q23-q24	KIAA0050 gene product	KIAA0050 gene product
HG2868-HT1	HG2868-HT1	HG2868-HT1	PASS	7	18.57	PASS	13	9	32.23	2.75	2.75	MCL1	1q21	transforming growth factor-beta	transforming growth factor-beta
MCL1	L08246_at	L08246	PASS	9	88.67	PASS	13	9	29.54	2.74	2.74			beclin 1 (coiled-coil, myosin-like BCL2-interacting protein)	beclin 1 (coiled-coil, myosin-like BCL2-interacting protein)
SI00A11	D38583 at	D38583	PASS	9	81.00	PASS	13	9	24.62	2.74	2.74	TNFRSF1B	1p36.3-p36.2	adenosine monophosphate deaminase 2 (isoform L)	adenosine monophosphate deaminase 2 (isoform L)
TNFR2	M32315_at	M32315	PASS	9	67.44	PASS	13	9	6.69	2.74	2.74				
NGG10	U31383_at	U31383	PASS	9	18.33	PASS	13	9	11.23	2.74	2.74	NGG10			
D38251_s at	D38251_s at	D38251	PASS	8	30.75	PASS	13	8	22.62	2.74	2.74	POLR2E	19p13.3		
K50_K41	D30758 at	D30758	PASS	9	61.89	PASS	13	9	22.62	2.74	2.74	KIAA0050			
M38449 s at	M38449 s at	M38449	PASS	6	33.50	PASS	8	6	12.25	2.73	2.73	TGF-beta			
GT197	L38932_at	L38932	PASS	9	40.33	PASS	13	9	14.77	2.73	2.73	BECN1			
AMPD2_cds	M91029_cds	M91029	PASS	9	30.33	PASS	13	9	11.15	2.72	2.72	AMPD2	1p13.3		

RABGGTA	Y08200_at	Y08200	PASS	9	23.56	PASS	12	9	8.67	2.72	2.72	RABGGTA	14q11.2	Rab geranylgeranyltransferase, alpha subunit	Rab geranylgeranyltransferase, alpha subunit
Y08682_ma	Y08682_ma	Y08682	PASS	9	13.56	PASS	8	9	5.00	2.71	2.71	CPT1B		canitine palmitoyltransferase 1	
MYH9	M31013_at	M31013	PASS	9	149.78	PASS	13	9	55.38	2.70	2.70	MYH9	22q12.3-q13.1	myosin, heavy polypeptide 9, non-muscle	
D00749_s_at	D00749_s_at	D00749	PASS	9	69.89	PASS	13	9	25.85	2.70	2.70			CD7 antigen	
U65416_ma	U65416_ma	U65416	PASS	9	17.33	PASS	12	9	6.42	2.70	2.70	MICB		MHC class I molecule	MHC class I chain-related gene B; cDNA sequence deposited under GenBank Accession Number X91625
Z22951_ma	Z22951_ma	Z22951	PASS	5	18.60	PASS	10	5	6.90	2.70	2.70	p65		p65 subunit of transcription factor NF-kappaB	
PRCC_ma	X99720_ma	X99720	PASS	7	22.43	PASS	9	7	8.33	2.69	2.69	TPRC			
HG2238-HT	HG2238-HT	HG2238-H	PASS	9	25.67	PASS	13	9	9.54	2.69	2.69				
SLC2A3	M20681_at	M20681	PASS	9	26.00	PASS	12	9	9.67	2.69	2.69	SLC2A3	12p13.3		solute carrier family 2 (facilitated glucose transporter), member 3
FCGR1	U12255_at	U12255	PASS	9	78.56	PASS	13	9	29.23	2.69	2.69	FCGR1	19q13.3	Fc fragment of IgG, receptor, transporter, alpha	
MAPT	HG2566-HT	HG2566-H	PASS	8	28.38	PASS	7	8	10.57	2.68	2.68				
E IFNGR2	U05875_at	U05875	PASS	8	34.88	PASS	8	8	13.00	2.68	2.68	AF-1			second chain of the receptor
TCFL1	D43642_at	D43642	PASS	9	38.22	PASS	13	9	14.31	2.67	2.67	YL-1		YL-1 protein	Nuclear protein with DNA-binding ability
U66711_ma	U66711_ma	U66711	PASS	8	48.75	PASS	12	8	18.25	2.67	2.67	LY6E	8q24.3	lymphocyte antigen 6 complex, locus E	
HVEM	U70321_at	U70321	PASS	9	28.11	PASS	13	9	10.54	2.67	2.67	TNFRSF14	1p36.3-p36.2	tumor necrosis factor receptor superfamily, member 14; herpesvirus entry mediator	
TPR2	U46571_at	U46571	PASS	9	17.78	PASS	12	9	6.67	2.67	2.67	TTC2	17q11.2	tetratricopeptide repeat domain 2	
GARS	U09587_at	U09587	PASS	9	29.67	PASS	13	9	11.15	2.66	2.66			glycyl-tRNA synthetase	
ARAF1	U01337_at	U01337	PASS	9	32.67	PASS	12	9	12.33	2.65	2.65	A-RAF-1		Ser/Thr protein kinase	cytoplasmic
ISGF3G	M87503_at	M87503	PASS	8	52.50	PASS	13	8	19.85	2.65	2.65	ISGF3-gamma		IFN-alpha responsive transcription factor	
PI	K01396_at	K01396	PASS	9	139.78	PASS	13	9	52.85	2.64	2.64	PI	14q32.1	protease inhibitor 1 (anti-elastase), alpha-1-antitrypsin	protease inhibitor 1 (anti-elastase)
BTG2	U72649_at	U72649	PASS	9	40.33	PASS	12	9	15.25	2.64	2.64	BTG2		rat PC3 and murine T1S21 genes homolog	
TXNRD1	U78678_at	U78678	PASS	8	20.25	PASS	9	8	7.67	2.64	2.64			thioredoxin	
CSNK2A2	M55268_at	M55268	PASS	9	17.33	PASS	7	9	6.57	2.64	2.64	CSNK2A2	16p13.3-p13.2	casein kinase 2, alpha prime polypeptide	casein kinase 2, alpha prime polypeptide
ARHG	X61587_at	X61587	PASS	9	51.89	PASS	13	9	19.69	2.63	2.63	ARHG	1p15.5-p15.4	ras homolog gene family, member G (rho G)	ras homolog gene family, member G (rho G)
IRF3	Z56281_at	Z56281	PASS	9	25.11	PASS	13	9	9.54	2.63	2.63	IRF3	19q13.3-q13.4	interferon regulatory factor 3	interferon regulatory factor 3
HEM1	M58285_at	M58285	PASS	9	38.44	PASS	13	9	14.62	2.63	2.63			membrane-associated protein	
NRAMP1	D50402_at	D50402	PASS	9	19.11	PASS	11	9	7.27	2.63	2.63	NRAMP1	2q35		natural resistance-associated macrophage protein 1 (might include Leishmaniasis)
CLAPB1	M34175_at	M34175	PASS	9	28.22	PASS	12	9	10.75	2.63	2.63	CLAPB1	17q11.2-q12	clathrin-associated/assembly/adaptor protein, large, beta 1	clathrin-associated/assembly/adaptor protein, large, beta 1
ZFP77	HG4332-HT	HG4332-H	PASS	8	14.63	PASS	7	8	5.57	2.63	2.63				
K151 SPK1	D63485_at	D63485	PASS	9	18.89	PASS	10	9	7.20	2.62	2.62	KIAA0151			KIAA0151 gene product

# Table 1

K226	D86979_at	D86979	PASS	9	20.56	PASS	13	9	7.85	2.62	2.62	KIAA0226			KIAA0226 gene product
BTN_mal	U97502_mal	U97502	PASS	6	16.50	PASS	13	6	6.31	2.62	2.62	BT3.3			butyrophilin
L32831_s_at	L32831_s_at	L32831	PASS	5	18.00	PASS	9	5	6.89	2.61	2.61				G protein-coupled receptor
FKBP4	M88279_at	M88279	PASS	9	23.11	PASS	13	9	8.85	2.61	2.61	FKBP4			FK506-binding protein 4 (59kD)
CTSD	M63138_at	M63138	PASS	9	82.89	PASS	12	9	31.75	2.61	2.61	CTSD			cathepsin D (lysosomal aspartyl protease)
HG23815-HT4	HG23815-HT4	HG23815-HT4	PASS	9	360.22	PASS	13	9	138.00	2.61	2.61				adaplin, beta 1 (beta prime)
L1939 s at	L1939 s at	L1939	PASS	8	24.88	PASS	13	8	9.54	2.61	2.61	ADTB1			acyloxycyl hydrolase (neutrophil)
AOAH	M62840_at	M62840	PASS	8	27.50	PASS	9	8	10.56	2.61	2.61	AOAH			acyloxycyl hydrolase (neutrophil)
TPR1	U46570_at	U46570	PASS	9	41.67	PASS	13	9	16.08	2.59	2.59	TTTC1			tetratricopeptide repeat domain 1
TUBA1	X01703_at	X01703	PASS	9	37.67	PASS	13	9	14.54	2.59	2.59				alpha-tubulin
CSR1	M62505_at	M62505	PASS	8	25.00	PASS	12	8	9.67	2.59	2.59	CSR1			complement component 5 receptor 1 (C5a ligand)
U43185_s_at	U43185_s_at	U43185	PASS	9	27.56	PASS	12	9	10.67	2.58	2.58	STAT5A			signal transducer and activator of transcription 5A
AARS	D32050_at	D32050	PASS	8	19.38	PASS	12	8	7.50	2.58	2.58	AARS			alanyl-tRNA synthetase
SREBF1	U00968_at	U00968	PASS	6	24.67	PASS	7	6	9.57	2.58	2.58	SREBF1			sterol regulatory element binding transcription factor 1
GIP2	M13755_at	M13755	PASS	7	30.71	PASS	13	7	11.92	2.58	2.58	ISG15			interferon-stimulated protein, 15 kDa
BCAT2	U62739_at	U62739	PASS	9	18.78	PASS	10	9	7.30	2.57	2.57	BCAT2			branched chain aminotransferase 2, mitochondrial
DCTD	L39874_at	L39874	PASS	8	26.38	PASS	11	8	10.27	2.57	2.57	DCTD			dCMP deaminase
K15_PPM1A	D13640_at	D13640	PASS	9	29.00	PASS	12	9	11.33	2.56	2.56	KIAA0015			KIAA0015 gene product
RTP	D87953_at	D87953	PASS	9	39.56	PASS	13	9	15.46	2.56	2.56	GC4			RTP
PXN	U14588_at	U14588	PASS	9	39.11	PASS	13	9	15.31	2.55	2.55	PXN			paxillin
KAP1_TIF1B	U95040_at	U95040	PASS	9	44.00	PASS	13	9	17.31	2.54	2.54				hKAP1/TIF1B
NRBTX	L20773_at	L20773	PASS	9	25.56	PASS	13	9	10.08	2.54	2.54				hyaluronoglucosaminidase 2
AJ000099 s	AJ000099 s	AJ000099	PASS	7	28.57	PASS	11	7	11.27	2.53	2.53	HYAL2			hyaluronoglucosaminidase 2
BZRP	L21954_at	L21954	PASS	9	127.89	PASS	13	9	50.46	2.53	2.53	BZRP			benzodiazepine receptor (peripheral)
HUK5	U67963_at	U67963	PASS	9	18.89	PASS	11	9	7.45	2.53	2.53	HUK5			lysophospholipase homolog
YF5	U84569_at	U84569	PASS	8	24.88	PASS	13	8	9.85	2.53	2.53	YF5			similar to A2 encoded by GenBank Accession Number U84570 and to sequence with GenBank Accession Number AC000020
STX5A	U26648_at	U26648	PASS	6	21.33	PASS	9	6	8.44	2.53	2.53	STX5A			synaptobrevin 5A
XG5784 s at	XG5784 s at	XG5784	PASS	8	21.88	PASS	12	8	8.67	2.52	2.52	CMAR			cell matrix adhesion regulator
SFCC13	L10910_at	L10910	PASS	9	16.11	PASS	13	9	6.38	2.52	2.52	CC1.3			splicing factor (CC1.3)
K79_CHR7	D38555_at	D38555	PASS	9	21.33	PASS	10	9	8.50	2.51	2.51	KIAA0079			Sec24p, S. Cerevisiae, homolog of
E_A9A2BRE	U00952_at	U00952	PASS	5	17.80	PASS	10	5	7.10	2.51	2.51				Sec24p, S. Cerevisiae, homolog of
LAG2	M85276_at	M85276	PASS	9	138.22	PASS	13	9	55.15	2.51	2.51	NGF5			NGF5 protein
M16750 s at	M16750 s at	M16750	PASS	9	34.89	PASS	13	9	13.92	2.51	2.51	PIM1			pim-1 oncogene
K120_NP25	D21261_at	D21261	PASS	9	278.78	PASS	13	9	111.31	2.50	2.50	TAGLN2			transgelin 2
PRKACG	U42412_at	U42412	PASS	8	16.38	PASS	11	8	6.55	2.50	2.50	PRKAG1			protein kinase, AMP-activated, gamma 1 non-catalytic subunit

# Table 1: F54E200T

U41315_ma	U41315_ma	U41315	PASS	9	15.00	PASS	11	9	6.00	2.50	2.50	ZNF127-Xp	ZNF127-Xp	ring zinc-finger protein; escapes X chromosome inactivation
NFI16	HG3494-HT	HG3494-H	PASS	9	80.56	PASS	13	9	32.23	2.50	2.50			annexin XI (56kD autoantigen)
ANX11	L19603	L19603	PASS	9	97.56	PASS	13	9	39.08	2.50	2.50	ANX11	10q22-q23	annexin XI (56kD autoantigen)
K25	D14695	D14695	PASS	8	17.88	PASS	12	8	7.17	2.49	2.49	KIAA0025		KIAA0025 gene product
K144	DAGK	D63478	PASS	7	13.43	PASS	13	7	5.38	2.49	2.49	KIAA0144		KIAA0144 gene product
S100A6	HG2788-HT	HG2788-H	PASS	9	179.22	PASS	13	9	72.15	2.48	2.48			ubiquitin-conjugating enzyme E2 variant 2
PUTDABP	U49278	U49278	PASS	8	27.63	PASS	13	8	11.15	2.48	2.48	UBE2V2		ubiquitin-conjugating enzyme E2 variant 2
HG3395-HT	HG3395-HT	HG3395-H	PASS	7	12.71	PASS	7	7	5.14	2.47	2.47			
BCL6	U00115	U00115	PASS	7	13.71	PASS	9	7	5.56	2.47	2.47	BCL6	3q27	B-cell CLL/lymphoma 6 (zinc finger protein 51)
SAFB	L43631	L43631	PASS	9	25.44	PASS	13	9	10.31	2.47	2.47	SAFB	19p13	scaffold attachment factor B
SRFGLYCP	Z50022	Z50022	PASS	8	32.00	PASS	13	8	13.00	2.46	2.46	C21ORF1	21q22.3	chromosome 21 open reading frame 1
MSN	M69066	M69066	PASS	9	178.78	PASS	13	9	72.85	2.45	2.45	MSN	Xq11.2-q12	moesin
PPP4C	X70218	X70218	PASS	7	27.43	PASS	11	7	11.18	2.45	2.45	PPP4C	16p12-16p11	protein phosphatase 4 (formerly X), catalytic subunit
EMP3	U52101	U52101	PASS	9	159.33	PASS	13	9	65.15	2.45	2.45	EMP3		epithelial membrane protein 3
TPH1	HG2279-HT	HG2279-H	PASS	9	73.33	PASS	13	9	30.00	2.44	2.44			
K121	D50911	D50911	PASS	9	16.44	PASS	11	9	6.73	2.44	2.44	KIAA0121		KIAA0121 gene product
M83652	s_a	M83652	PASS	9	46.56	PASS	13	9	19.08	2.44	2.44	PPC	Xp11.4	properdin P factor, complement
PLBK	U78095	U78095	PASS	5	26.40	PASS	11	5	10.82	2.44	2.44			member of the Kunitz family of protease inhibitors
FKBP1	M34539	M34539	PASS	9	42.78	PASS	13	9	17.54	2.44	2.44	FKBP1A	20p13	FK506-binding protein 1A (12kD)
S100A4	M80563	M80563	PASS	9	213.22	PASS	13	9	87.62	2.43	2.43	S100A4	1q12-q22	S100 calcium-binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homologue)
UQCRC1	L16842	L16842	PASS	9	24.11	PASS	12	9	9.92	2.43	2.43	UQCRC1	3p21	ubiquinol-cytochrome c reductase core protein 1
Y10807	s_at	Y10807	PASS	7	35.14	PASS	13	7	14.46	2.43	2.43	HRMT1L2	19q13	HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2
SELP	M25322	M25322	PASS	9	15.00	PASS	11	9	6.18	2.43	2.43	SELP	1q22-q25	selectin P (granule membrane protein 140kD, antigen CD62)
PTGS1	M59979	M59979	PASS	8	15.25	PASS	7	8	6.29	2.43	2.43	PTGS1	9q32-q33.3	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)
PIL	U46751	U46751	PASS	9	98.78	PASS	13	9	40.77	2.42	2.42	P62		UBIQUITIN-BINDING PROTEIN P62; phosphotyrosine independent ligand for the Lck SH2 domain p62
ITPK1	U51336	U51336	PASS	9	49.00	PASS	13	9	20.23	2.42	2.42			inositol 1,3,4-trisphosphate 5/6-kinase
KNS2	L04733	L04733	PASS	7	17.29	PASS	7	7	7.14	2.42	2.42			putative
M23323	s_a	M23323	PASS	9	45.78	PASS	13	9	18.92	2.42	2.42	CD3E	11q23	CD3E antigen, epsilon polypeptide (T1T3 complex)
X76223	s_at	X76223	PASS	7	36.86	PASS	12	7	15.25	2.42	2.42	MAL	2cen-q13	mal, T-cell differentiation protein

# FOETAL T ESTEROID

OS9	U41635_at	U41635	PASS	9	58.56	PASS	13	9	24.23	2.42	2.42			OS-9 precursor	ubiquitously expressed in human tissues and amplified in sarcomas
RP66KA2	L07597_at	L07597	PASS	9	28.78	PASS	12	9	11.92	2.41	2.41	3	RPS6KA1	ribosomal protein S6 kinase, 90kD, polypeptide 1	
IFNG	L07633_at	L07633	PASS	9	84.33	PASS	13	9	34.92	2.41	2.41		PSME1	interferon-gamma	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)
FRAPL	L37033_at	L37033	PASS	8	29.38	PASS	11	8	12.18	2.41	2.41		FKBP38	FK-506 binding protein	
CES1	L07765_at	L07765	PASS	7	15.43	PASS	10	7	6.40	2.41	2.41	16q13-q22.1	CES1	homologue carboxylesterase 1 (monocyte/macrophage serine esterase 1)	carboxylesterase 1 (monocyte/macrophage serine esterase 1)
X56681 s at	X56681 s at	X56681	PASS	9	114.44	PASS	13	9	47.54	2.41	2.41	19p13.2	JUND	high density lipoprotein binding protein	Jun D proto-oncogene
HDLBP	M64098_at	M64098	PASS	8	20.00	PASS	13	8	8.31	2.41	2.41		HBP	protein	
ECGF1_ma3	L62317_ma3	L62317	PASS	9	66.22	PASS	13	9	27.54	2.40	2.40			arylsulfatase A	hypothetical protein 384D8 2
K140	D50930_at	D50930	PASS	8	18.13	PASS	11	8	7.55	2.40	2.40		KIAA0140		KIAA0140 gene product
HG4541-HT4	HG4541-HT4	HG4541-HT4	PASS	9	41.56	PASS	13	9	17.31	2.40	2.40				
ARP	M83751_at	M83751	PASS	9	21.22	PASS	13	9	8.85	2.40	2.40		ARP	arginine-rich protein	putative
HG417-HT4	HG417-HT4	HG417-HT4	PASS	9	71.33	PASS	13	9	29.77	2.40	2.40				
STM	U20499_at	U20499	PASS	9	20.33	PASS	12	9	8.50	2.39	2.39	16p11.2	SULT1A3	thermolabile phenol sulfotransferase	sulfotransferase family 1A, phenol-preferring, member 3
NP	K02574_at	K02574	PASS	8	32.88	PASS	13	8	13.77	2.39	2.39	14q11.2	NP	nucleoside phosphorylase	nucleoside phosphorylase
GLA	X14448_at	X14448	PASS	9	20.56	PASS	13	9	8.62	2.39	2.39			alpha-D-galactosidase A	
ARNP	M74002_at	M74002	PASS	9	20.00	PASS	13	9	8.38	2.39	2.39	1p21-p34	SPRS11	splicing factor, arginine/serine-rich 11	splicing factor, arginine/serine-rich 11
K168	D79990_at	D79990	PASS	9	29.33	PASS	13	9	12.31	2.38	2.38		KIAA0168	suppressor of Ty (S.cerevisiae)	KIAA0168 gene product
SUPT4H1	U43923_at	U43923	PASS	8	21.63	PASS	12	8	9.08	2.38	2.38	17q21-q23	SUPT4H1	homolog 1	suppressor of Ty (S.cerevisiae) 4 homolog 1
K174	D79996_at	D79996	PASS	9	28.56	PASS	13	9	12.00	2.38	2.38		KIAA0174	D-dopachrome tautomerase	KIAA0174 gene product
DCT	U49785_at	U49785	PASS	9	24.89	PASS	13	9	10.46	2.38	2.38	22q11.2	DDT	carboxyl terminal LIM domain protein	D-dopachrome tautomerase
CLP36	U90878_at	U90878	PASS	9	26.56	PASS	12	9	11.17	2.38	2.38	10q22-q27	CLIM1	lysosomal-associated multitransmembrane protein	carboxyl terminal LIM domain protein 1
LAMP5	U51240_at	U51240	PASS	9	146.89	PASS	13	9	61.77	2.38	2.38		LAPTM5	natural killer cell transcript 4	lysosomal-associated multitransmembrane protein
NK4	M59807_at	M59807	PASS	9	116.67	PASS	13	9	49.15	2.37	2.37	16p13.3	NK4	natural killer cell transcript 4	natural killer cell transcript 4
K223_COSZ	D86976_at	D86976	PASS	9	103.11	PASS	13	9	43.46	2.37	2.37		KIAA0223	B94 protein	similar to C elegans protein (Z37093)
B94	M92357_at	M92357	PASS	9	27.00	PASS	13	9	11.38	2.37	2.37			secreted protein, acidic, cysteine-rich (osteonectin)	secreted protein, acidic, cysteine-rich (osteonectin)
SPARC	J03040_at	J03040	PASS	9	57.78	PASS	13	9	24.38	2.37	2.37	5q31-q33	SPARC	protective protein for beta-galactosidase	protective protein for beta-galactosidase (galactosialidosis)
PPGB	M22960_at	M22960	PASS	9	83.44	PASS	13	9	35.23	2.37	2.37	20q13.1	PPGB	interferon-induced Mx protein	galactosidase (galactosialidosis) myxovirus (influenza) resistance 2, homolog of murine
MX2	M30818_at	M30818	PASS	9	20.56	PASS	13	9	8.69	2.36	2.36	21q22.3	MX2	silencing mediator of retinoid and thyroid hormone action	transcriptional co-repressor
SMRT	U37146_at	U37146	PASS	9	26.56	PASS	13	9	11.23	2.36	2.36		SMRT	diacylglycerol kinase, zeta (104kD)	diacylglycerol kinase, zeta (104kD)
DGK5Z	U51477_at	U51477	PASS	9	32.56	PASS	13	9	13.77	2.36	2.36		DGKZ	lysosomal membrane glycoprotein-1	precursor
LAMP1	J04182_at	J04182	PASS	9	47.78	PASS	13	9	20.23	2.36	2.36		LAMP1	hexokinase 3 (white cell)	hexokinase 3 (white cell)
YWHAE	U54778_at	U54778	PASS	8	14.50	PASS	13	8	6.15	2.36	2.36				
U51333 s at	U51333 s at	U51333	PASS	9	47.11	PASS	13	9	20.00	2.36	2.36	5q35.2	HK3		



# Table 2

CRFB4	Z17227_at	Z17227	PASS	9	15.78	PASS	10	9	6.70	2.35	2.35	2.35	IL10RB	21q22.1-q22.2	interleukin 10 receptor, beta	interleukin 10 receptor, beta
PIM2	U77735_at	U77735	PASS	6	24.33	PASS	12	6	10.33	2.35	2.35	2.35			pim-2 protooncogene homolog	pim-2 protooncogene homolog
AAMP	M95627_at	M95627	PASS	9	22.11	PASS	12	9	9.42	2.35	2.35	2.35	AAMP		angio-associated, migratory cell protein	angio-associated, migratory cell protein
K67_TQ2	D31891_at	D31891	PASS	9	18.56	PASS	11	9	7.91	2.35	2.35	2.35	KIAA0067		KIAA0067 gene product	KIAA0067 gene product
NKG2D	X54870_at	X54870	PASS	9	31.33	PASS	13	9	13.38	2.34	2.34	2.34	NKG2-D gene		Type II integral membrane protein	Type II integral membrane protein
M81695_s_a	M81695_s_a	M81695	PASS	9	32.22	PASS	13	9	13.77	2.34	2.34	2.34	ITGAX	16p13.1-p11	integrin, alpha X (antigen CD11C (p150), alpha polypeptide)	integrin, alpha X (antigen CD11C (p150), alpha polypeptide)
KRT12	U77643_at	U77643	PASS	8	28.25	PASS	13	8	12.08	2.34	2.34	2.34	SECTM1	17q25	secreted and transmembrane 1	secreted and transmembrane 1
LGALS9	AB006782_a	AB006782	PASS	9	78.89	PASS	13	9	33.77	2.34	2.34	2.34	LGALS9		lectin, galactoside-binding, soluble, 9 (galactin 9)	lectin, galactoside-binding, soluble, 9 (galactin 9)
ARF3	M74491_at	M74491	PASS	9	54.11	PASS	13	9	23.23	2.33	2.33	2.33	ARF3	12q13	ADP-ribosylation factor 3	ADP-ribosylation factor 3
ALDH7	U10868_at	U10868	PASS	8	16.88	PASS	12	8	7.25	2.33	2.33	2.33	ALDH7	11q13	aldehyde dehydrogenase 7	aldehyde dehydrogenase 7
M54915_s_a	M54915_s_a	M54915	PASS	9	54.67	PASS	13	9	23.54	2.32	2.32	2.32	FAH	15q23-q25	funarylacetate	funarylacetate
TPM3	M55150_at	M55150	PASS	6	18.50	PASS	8	6	8.00	2.31	2.31	2.31	FAH	8p21.1	focal adhesion kinase 2 (protein kinase B)	focal adhesion kinase 2 (protein kinase B)
CAKB	U43522_at	U43522	PASS	8	14.13	PASS	9	8	6.11	2.31	2.31	2.31	PTK2B	19p13.3-p13.2	intercellular adhesion molecule 3	intercellular adhesion molecule 3
ICAM3	X69819_at	X69819	PASS	9	52.22	PASS	13	9	22.62	2.31	2.31	2.31	ICAM3	7q32	interferon regulatory factor 5	interferon regulatory factor 5
IRF5	U51127_at	U51127	PASS	9	29.00	PASS	7	9	12.57	2.31	2.31	2.31	IRF5		adenyl cyclase-associated protein	adenyl cyclase-associated protein
CAP	L12168_at	L12168	PASS	9	134.67	PASS	13	9	58.38	2.31	2.31	2.31	CAP	17q11.1-q11.2	TATA box binding protein (TBP)-associated factor, RNA polymerase II, N, 68kD (RNA-binding protein 56)	TATA box binding protein (TBP)-associated factor, RNA polymerase II, N, 68kD (RNA-binding protein 56)
RBP56	U51334_at	U51334	PASS	8	25.50	PASS	13	8	11.08	2.30	2.30	2.30	TAF2N		heat shock protein	heat shock protein
HSPA1L	M11717_ma	M11717	PASS	9	53.11	PASS	13	9	23.08	2.30	2.30	2.30	HSPA1L		RalGDS-like	RalGDS-like
RGL2	U68142_at	U68142	PASS	9	15.67	PASS	11	9	6.82	2.30	2.30	2.30	RGL2		pms5 protein	pms5 protein
PM5	X57398_at	X57398	PASS	9	27.33	PASS	12	9	11.92	2.29	2.29	2.29	PM5		protein sequence is in conflict with the conceptual translation	protein sequence is in conflict with the conceptual translation
K217	D86971_at	D86971	PASS	5	17.20	PASS	10	5	7.50	2.29	2.29	2.29	KIAA0217		no similarities to reported gene products	no similarities to reported gene products
CAPG	M94345_at	M94345	PASS	9	49.33	PASS	13	9	21.54	2.29	2.29	2.29	CAPG	2cen-q24	capping protein (actin filament), gelsolin-like	capping protein (actin filament), gelsolin-like
PIN1	U49070_at	U49070	PASS	6	14.50	PASS	12	6	6.33	2.29	2.29	2.29	PIN1		NIMA-interacting protein 1, essential mitotic regulator, essential peptidyl-prolyl isomerase	NIMA-interacting protein 1, essential mitotic regulator, essential peptidyl-prolyl isomerase
U72882_s_at	U72882_s_at	U72882	PASS	6	15.50	PASS	9	6	6.78	2.29	2.29	2.29	IFP15		interferon-induced leucine zipper protein	interferon-induced leucine zipper protein
ITGAM	J03925_at	J03925	PASS	9	23.56	PASS	13	9	10.31	2.29	2.29	2.29	ITGAM	16p11.2	integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide)	integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide)
IQGAP2	U51903_at	U51903	PASS	8	17.38	PASS	13	8	7.62	2.28	2.28	2.28	IQGAP2		RasGAP-related protein	RasGAP-related protein

# Table 1

MLN62	X80200_at	X80200	PASS	9	15.11	PASS	8	9	6.63	2.28	2.28	17q11-q12	TNF receptor-associated factor 4	TNF receptor-associated factor 4	
INPP5D	U57650_at	U57650	PASS	9	42.78	PASS	13	9	18.77	2.28	2.28	2q36-q37	SH2-containing inositol 5-phosphatase	inositol polyphosphate-5-phosphatase, 145kD	
M13829_s_a	M13829_s_a	M13829	PASS	8	15.25	PASS	13	8	6.69	2.28	2.28	Xp11.4-p11.2	v-rat murine sarcoma 3611 viral oncogene homolog 1	v-rat murine sarcoma 3611 viral oncogene homolog 1	
ITGB2	M15395_at	M15395	PASS	9	86.11	PASS	13	9	37.85	2.28	2.28	21q22.3	integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit)	integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit)	
D43682_s_at	D43682_s_at	D43682	PASS	9	41.44	PASS	13	9	18.23	2.27	2.27	17p13-p11	acyl-Coenzyme A dehydrogenase, very long chain	acyl-Coenzyme A dehydrogenase, very long chain	
FTTH	L20941_at	L20941	PASS	9	279.00	PASS	13	9	122.77	2.27	2.27	11q13	ferritin, heavy polypeptide 1	ferritin, heavy polypeptide 1	
PSMHC9	D00763_at	D00763	PASS	9	42.78	PASS	12	9	18.83	2.27	2.27	PSMA4	proteasome (prosome, macropain) subunit, alpha type, 4	proteasome (prosome, macropain) subunit, alpha type, 4	
AKT1	M63167_at	M63167	PASS	8	23.13	PASS	11	8	10.18	2.27	2.27	14q32.3	rac protein kinase-alpha	v-akt murine thymoma viral oncogene homolog 1	
POGA	L24783_at	L24783	PASS	7	14.29	PASS	10	7	6.30	2.27	2.27				
K106_B15C	D14662_at	D14662	PASS	9	36.44	PASS	13	9	16.08	2.27	2.27	1	anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent phospholipase A2)	anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent phospholipase A2)	
CYP2A6_f	X13930_f_at	X13930	PASS	5	13.60	PASS	9	5	6.00	2.27	2.27			P-450 1A4 protein (AA 1-494)	
K113	D30755_at	D30755	PASS	9	29.11	PASS	13	9	12.85	2.27	2.27	19q13.13	guanidine nucleotide exchange factor; 115-kD; mouse Lsc homolog	guanidine nucleotide exchange factor; 115-kD; mouse Lsc homolog	
P115RHOGH	U64105_at	U64105	PASS	9	43.56	PASS	13	9	19.23	2.26	2.26		transaldolase	transaldolase	
TALDO1	L19437_at	L19437	PASS	9	85.33	PASS	13	9	37.69	2.26	2.26		proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	
PSMD2	D78151_at	D78151	PASS	9	36.22	PASS	13	9	16.00	2.26	2.26		lectin, galactoside-binding, soluble, 1 (galectin 1)	lectin, galactoside-binding, soluble, 1 (galectin 1)	
LGALS1	J04456_at	J04456	PASS	9	102.89	PASS	13	9	45.46	2.26	2.26	22q12-q13	ubiquitin fusion-degradation 1 like protein	ubiquitin fusion-degradation 1 like protein	
UF01L	U64444_at	U64444	PASS	9	22.78	PASS	13	9	10.08	2.26	2.26				
K68	D38549_at	D38549	PASS	8	19.63	PASS	10	8	8.70	2.26	2.26		ha1025 is new	ha1025 is new	
PBX1	M86546_at	M86546	PASS	6	12.50	PASS	11	6	5.55	2.25	2.25	1q23	pre-B-cell leukemia transcription factor 1	pre-B-cell leukemia transcription factor 1	
RAC2	HG1102-HT	HG1102-HT	PASS	9	20.11	PASS	13	9	8.92	2.25	2.25			protein kinase, mitogen-activated, kinase 2, p45 (MAP kinase kinase 2)	protein kinase, mitogen-activated, kinase 2, p45 (MAP kinase kinase 2)
PRKMK2	L11285_at	L11285	PASS	9	29.11	PASS	13	9	12.92	2.25	2.25			This gene is novel.	This gene is novel.
K82_ACNP	D43949_at	D43949	PASS	8	16.75	PASS	11	8	7.45	2.25	2.25		paired basic amino acid cleaving system 4	paired basic amino acid cleaving system 4	
PACE4	M80482_at	M80482	PASS	7	11.71	PASS	9	7	5.22	2.24	2.24	15q26		This sequence comes from Fig. 3.	
GMCSFIND	S69115_at	S69115	PASS	8	80.38	PASS	13	8	35.85	2.24	2.24		granulocyte colony-stimulating factor induced gene		

[illegible]

Z47038_s_at	Z47038_s_at	Z47038	PASS	8	12.88	PASS	11	8	5.91	2.18	2.18	putative microtubule associated protein 1A		open reading frame; N-terminal region
K224 DDX	D86977_at	D86977	PASS	8	15.25	PASS	13	8	7.00	2.18	2.18	KIAA0224		KIAA0224 gene product
K160	D63881_at	D63881	PASS	9	14.56	PASS	13	9	6.69	2.17	2.17	KIAA0160		KIAA0160 gene product is novel.
D83260_s_at	D83260_s_at	D83260	PASS	9	16.56	PASS	13	9	7.62	2.17	2.17	DXS9928E	Xq28	putative candidate disease gene
EIF3	U78525_at	U78525	PASS	9	19.56	PASS	13	9	9.00	2.17	2.17	EIF3S9		putative candidate disease gene
K169	D79991_at	D79991	PASS	9	13.67	PASS	10	9	6.30	2.17	2.17	KIAA0169		putative candidate disease gene
GZMA_ma1	M18737_ma	M18737	PASS	9	75.22	PASS	13	9	34.69	2.17	2.17	GZMA	5q11-q12	putative hydrophobic domain in amino acid positions 373-390.
PPP1	U14603_at	U14603	PASS	9	76.56	PASS	13	9	35.31	2.17	2.17	PTP4A2	1p35	protein tyrosine phosphatase type IVA, member 2
MLF2	U57342_at	U57342	PASS	9	26.00	PASS	13	9	12.00	2.17	2.17	MLF2		myelodysplasia/myeloid leukemia factor 2
M84371_ma	M84371_ma	M84371	PASS	8	14.38	PASS	11	8	6.64	2.17	2.17	CD19		
H1X	D64142_at	D64142	PASS	9	54.89	PASS	13	9	25.38	2.16	2.16	H1FX		H1 histone family, member X
CMKBR2_ma	U95626_ma	U95626	PASS	8	36.75	PASS	13	8	17.00	2.16	2.16	CCR2		confirmed by similarity to Human monocyte chemoattractant protein 1 receptor (CCR2) alternatively spliced A-form. Encoded by GenBank Accession Number U80924, gi 1168965
U32986_s_at	U32986_s_at	U32986	PASS	9	24.67	PASS	12	9	11.42	2.16	2.16	DDB1	11q12-q13	damage-specific DNA binding protein 1 (127kD)
MPP1	M64925_at	M64925	PASS	9	34.89	PASS	12	9	16.17	2.16	2.16	MPP1	Xq28	membrane protein, palmitoylated 1 (55kD)
BCL2	M14745_at	M14745	PASS	9	16.22	PASS	13	9	7.54	2.15	2.15			bcl-2 protein
DAGK1	X62535_at	X62535	PASS	9	38.56	PASS	13	9	17.92	2.15	2.15	DGKA	12	diacylglycerol kinase (80kD)
M63438_s_at	M63438_s_at	M63438	PASS	9	167.11	PASS	13	9	77.77	2.15	2.15	TRADD		
TRADD	L41690_at	L41690	PASS	9	18.00	PASS	13	9	8.38	2.15	2.15			tumor necrosis factor receptor type 1 associated protein
PGM1	M83088_at	M83088	PASS	9	16.67	PASS	13	9	7.77	2.15	2.15	PGM1	1p22.1	phosphoglucomutase 1
CRIP1	U09770_at	U09770	PASS	9	35.33	PASS	12	9	16.50	2.14	2.14	hCRHP		cysteine-rich heart protein
K43 HOM	D26362_at	D26362	PASS	8	17.13	PASS	9	8	8.00	2.14	2.14	KIAA0043		KIAA0043 gene product
MYD88	U70451_at	U70451	PASS	8	38.13	PASS	13	8	17.85	2.14	2.14	MYD88	3p22	myeloid differentiation primary response gene (88)
HNRPH1	L22009_at	L22009	PASS	9	74.00	PASS	13	9	34.69	2.13	2.13			49 kDa protein; heterogeneous nuclear ribonucleoprotein H
MXI1	L07648_at	L07648	PASS	9	17.56	PASS	13	9	8.23	2.13	2.13	MXI1		
GUK1	L76200_at	L76200	PASS	8	56.25	PASS	13	8	26.38	2.13	2.13	GUK1	1q32-q42	guanylate kinase 1
CRFPH	AJ000480_at	AJ000480	PASS	5	11.60	PASS	9	5	5.44	2.13	2.13	CRFW		phosphoprotein
GNG11	U31384_at	U31384	PASS	9	38.78	PASS	13	9	18.23	2.13	2.13	GNG11		guanine nucleotide binding protein 11
HG3076-HTT	HG3076-HTT	HG3076-H	PASS	9	52.33	PASS	13	9	24.62	2.13	2.13			
UGT2B4	U03105_at	U03105	PASS	7	19.86	PASS	11	7	9.36	2.12	2.12			B4-2 protein

DPYSL2	U97105 at D29805	U97105 at D29805	PASS	8	18.75	PASS	13	8	2.12	2.12	2.12	DPYSL2	8p22-p21	dhhydropyrimidinase-like 2
GGTB2	D29805_at	D29805	PASS	9	40.89	PASS	13	9	19.31	2.12	2.12	B4GALT1	9p13	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1
M61827_ma	M61827_ma	M61827	PASS	9	33.22	PASS	10	9	15.70	2.12	2.12	SPN		leukosialin
D63479_s_at	D63479_s_at	D63479	PASS	9	18.67	PASS	12	9	8.83	2.11	2.11	DGKD		diacylglycerol kinase, delta (130kD)
IP	L47738_at	L47738	PASS	9	29.22	PASS	12	9	13.83	2.11	2.11	VASP	19q13.2-q13.3	inducible protein vasodilator-stimulated phosphoprotein
X98534_s_at	X98534_s_at	X98534	PASS	8	25.50	PASS	13	8	12.08	2.11	2.11			serine/threonine protein kinase
CALM1	HG1862-HT	HG1862-HT	PASS	9	91.11	PASS	13	9	43.15	2.11	2.11	HPK1		FK506-binding protein 2 (13kD)
HPK1	U66464_at	U66464	PASS	9	16.89	PASS	13	9	8.00	2.11	2.11	FKBP2	11q13.1-q13.3	chemokine (C-C motif) receptor 7
FKBP2	M75099_at	M75099	PASS	9	23.56	PASS	12	9	11.17	2.11	2.11	CCR7	17q12-q21.2	G protein-coupled receptor kinase 6
CMKBR7	L31584_at	L31584	PASS	9	39.89	PASS	13	9	18.92	2.11	2.11	GPRK6	5q35	Fe fragment of IgE, high affinity I, receptor for; gamma polypeptide
GPRK6	L16862_at	L16862	PASS	7	25.29	PASS	7	7	12.00	2.11	2.11	FCER1G	1q23	interleukin-1 receptor-associated kinase 1
FCER1G	M33195_at	M33195	PASS	9	112.00	PASS	13	9	53.15	2.11	2.11			phosphatidylinositol 4-kinase, catalytic, beta polypeptide
MRP	HG1612-HT	HG1612-HT	PASS	8	20.00	PASS	12	8	9.50	2.11	2.11	LYL1		tumor necrosis factor receptor superfamily, member 1A
LYL1	M22638_at	M22638	PASS	8	14.38	PASS	12	8	6.83	2.10	2.10	IRAK1	Xq28	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)
IRAK1	L76191_at	L76191	PASS	9	32.67	PASS	13	9	15.54	2.10	2.10	PIK4CB	1q21	cytoskeleton-associated protein 1
PI4KB	U81802_at	U81802	PASS	7	14.71	PASS	11	7	7.00	2.10	2.10	GT335		serum response factor (c-fos serum response element-binding transcription factor)
GT335	U53003_at	U53003	PASS	9	12.22	PASS	11	9	5.82	2.10	2.10	TNFRSF1A	12p13.2	adenylate cyclase activating polypeptide 1 (pituitary)
M58286_s_at	M58286_s_at	M58286	PASS	7	17.43	PASS	10	7	8.30	2.10	2.10	PSME2	14q11.2	vinculin
PSMA28	D45248_at	D45248	PASS	9	69.44	PASS	13	9	33.08	2.10	2.10	CKAP1	19q13.11-q13.12	calmodulin
CKAP1	D49738_at	D49738	PASS	9	34.56	PASS	13	9	16.46	2.10	2.10	SRF		synaptobrevin binding protein 1
HG4334-HT	HG4334-HT	HG4334-HT	PASS	6	14.50	PASS	12	6	6.92	2.10	2.10	hCKA alpha		coatomer protein complex, subunit alpha
SRF	J03161_at	J03161	PASS	6	18.83	PASS	9	6	9.00	2.09	2.09	ADCYAP1	18p11	damage-specific DNA binding protein 2 (48kD)
CRAA	U78556_at	U78556	PASS	8	15.75	PASS	13	8	7.54	2.09	2.09	VCL	10q11.2-qter	motilin
S83513_s_at	S83513_s_at	S83513	PASS	7	11.14	PASS	9	7	5.33	2.09	2.09	KIAA0183		
VCL	M33308_at	M33308	PASS	9	50.22	PASS	13	9	24.08	2.09	2.09	CALM1		
K183	D80005_at	D80005	PASS	9	25.00	PASS	13	9	12.00	2.08	2.08	STXBP1	9q34.1	
J04046_s_at	J04046_s_at	J04046	PASS	8	29.13	PASS	12	8	14.00	2.08	2.08	COPA		
STXBP3	D63851_at	D63851	PASS	5	9.80	PASS	7	5	4.71	2.08	2.08	DD2	11p12-p11	
COPA	U24105_at	U24105	PASS	9	36.78	PASS	13	9	17.69	2.08	2.08			
DD2	U18300_at	U18300	PASS	9	12.11	PASS	12	9	5.83	2.08	2.08			
MLN_ma1	X15393_ma1	X15393	PASS	7	13.29	PASS	10	7	6.40	2.08	2.08			



# TABLE "T" THE200F

ETR3	U69546_at	U69546	PASS	7	22.71	PASS	13	7	11.15	2.04	2.04	2.04	Err-3	protein contains 3 RRM motifs that may bind RNA; putative RNA binding protein; Elav-type ribonucleoprotein; complete sequence of human EST, Genbank Accession Number R57293
GSK3A	L40027_at	L40027	PASS	9	19.89	PASS	13	9	9.77	2.04	2.04	2.04	glycogen synthase kinase 3	exon 1 part (leader region): bp6-77; exon 2 part (alpha-1 domain): bp78-347; exon 3 part (alpha-2 domain): bp348-623; exon 4 part (alpha-3 domain): bp624-899; exon 5 part (transmembrane region): bp900-1016; exon 6 part (cytoplasmic region): bp1017-1049; exon 7 part (cytoplasmic region): bp1050-1097; exon 8 part (cytoplasmic region): bp1098-1103
HLA-A_f	D32129_f_at	D32129	PASS	9	342.11	PASS	13	9	168.23	2.03	2.03	2.03	HLA-A26	
RBI	L22343_at	L22343	PASS	7	12.86	PASS	9	7	6.33	2.03	2.03	2.03	nuclear phosphoprotein	IFN-induced
PIK4	L36151_at	L36151	PASS	9	39.89	PASS	13	9	19.69	2.03	2.03	2.03	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide
SPS2	U43286_at	U43286	PASS	9	13.67	PASS	12	9	6.75	2.02	2.02	2.02	selenophosphate synthetase 2	the amino acid residue number 60 is a selenocysteine encoded by the TGA (UGA) codon; We designated this enzyme selenophosphate synthetase 2 to distinguish it from the human homolog described by Low, S.C., Hamley, J.W. and Berry, M.J. J. Biol. Chem. 270, 21659-21664 (1995) (GenBank Accession Number U34044)
HYPA	U81556_at	U81556	PASS	9	40.44	PASS	13	9	20.00	2.02	2.02	2.02	hypothetical protein A4	
3PK	U09578_at	U09578	PASS	8	17.25	PASS	13	8	8.54	2.02	2.02	2.02	MAPKAPK 3	mitogen-activated protein kinase-activated protein kinase 3
K23_CAN	D14689_at	D14689	PASS	9	32.11	PASS	12	9	15.92	2.02	2.02	2.02	KIAA0023	KIAA0023 gene product
RNA_OSTB	AB000115_a	AB000115	PASS	7	12.86	PASS	8	7	6.38	2.02	2.02	2.02		The submiters designated this product as GS3686
IL2RG	D11086_at	D11086	PASS	9	42.00	PASS	13	9	20.85	2.01	2.01	2.01	IL2RG	interleukin 2 receptor, gamma (severe combined immunodeficiency)
SEC14L	D67029_at	D67029	PASS	5	15.60	PASS	12	5	7.75	2.01	2.01	2.01	SEC14L	SEC14 (S. cerevisiae)-like
POLG	U60325_at	U60325	PASS	6	13.33	PASS	8	6	6.63	2.01	2.01	2.01	POLG	polymerase (DNA directed), gamma
K142_K6	D63476_at	D63476	PASS	9	14.22	PASS	13	9	7.08	2.01	2.01	2.01	P85SPR	PAK-interacting exchange factor
FCGR1A	M63835_at	M63835	PASS	7	12.29	PASS	8	7	6.13	2.01	2.01	2.01	FCGR1A	beta
MLK3	L32976_at	L32976	PASS	7	12.29	PASS	7	7	6.14	2.00	2.00	2.00	IgG Fc receptor 1	Fc fragment of IgG, high affinity Ia, receptor for (CD64)
E_CCA12	U06681_at	U06681	PASS	5	12.40	PASS	10	5	6.20	2.00	2.00	2.00	MLK3	mixed lineage kinase 3

# FOETAL T54E200T

FACL1	D10040_at	D10040	PASS	5	12.00	PASS	9	5	6.00	2.00	2.00	FACL1	3q13	fatty-acid-Coenzyme A ligase, long-chain 1	fatty-acid-Coenzyme A ligase, long-chain 1
MCM6	D84557_at	D84557	PASS	9	13.44	PASS	11	9	6.73	2.00	2.00			HsMcm6	
BRCA2	U50523_at	U50523	PASS	9	84.89	PASS	13	9	42.54	2.00	2.00				
BIOC3	AFEX-BioC-1	AFEX-BioC-1	fail	4		PASS	13	4	14.46	Normal	Normal				
L15189_s_at	L15189_s_at	L15189	fail	4		PASS	13	4	6.77	Normal	Normal	HSPA9B	5q31.1	heat shock 70KD protein 9B (mortalin-2)	heat shock 70KD protein 9B (mortalin-2)
NIP71	U83843_at	U83843	fail	4		PASS	13	4	6.77	Normal	Normal	Nip7-1		HIV-1 Nef interacting protein	similar to murine CCT (chaperonin containing TCP-1) eta subunit encoded by GenBank Accession Number Z31399; CCT assists the folding of proteins in eukaryotic cytosol; Nef enhances the infectivity of HIV and SIV
APT1	D49396_at	D49396	fail	4		PASS	13	4	4.85	Normal	Normal			Aop1_Human, MERS(Aop1_Mouse)-like protein	
RAB1	M28209_at	M28209	fail	3		PASS	13	3	6.23	Normal	Normal	RAB1	2p14-p13.4	RAB1, member RAS oncogene family	RAB1, member RAS oncogene family
M28213_s_at	M28213_s_at	M28213	fail	3		PASS	13	3	5.77	Normal	Normal	RAB2		RAB2, member RAS oncogene family	RAB2, member RAS oncogene family
L00634_s_at	L00634_s_at	L00634	fail	2		PASS	13	2	6.15	Normal	Normal	FNTA	8p22-q11	farnesyltransferase, CAAAX box, alpha	farnesyltransferase, CAAAX box, alpha
PEPD	J04605_at	J04605	fail	2		PASS	13	2	5.38	Normal	Normal	PEPD	19q12-q13.2	peptidase D	peptidase D
SEC7PL	U59752_at	U59752	fail	4		PASS	12	4	7.92	Normal	Normal	PSCD2		pleckstrin homology, Sec7 and coiled/coil domains 2 (cytohesin-2)	pleckstrin homology, Sec7 and coiled/coil domains 2 (cytohesin-2)
K112	D25218_at	D25218	fail	4		PASS	12	4	6.42	Normal	Normal	KIAA0112		transcription elongation factor A (SII)-like 1	transcription elongation factor A (SII)-like 1
PP21	M99701_at	M99701	fail	4		PASS	12	4	5.75	Normal	Normal	TCEAL1	Xq22.1		
AFEX-BioB-2	AFEX-BioB-2	AFEX-BioB-2	fail	3		PASS	12	3	10.75	Normal	Normal	CREBBP	16p13.3	CREB binding protein (Rubinstein-Taybi syndrome)	CREB binding protein (Rubinstein-Taybi syndrome)
E_CREBBP	U89355_at	U89355	fail	3		PASS	12	3	5.17	Normal	Normal	CUL1		culin 1	culin 1
CUL1	U58087_at	U58087	fail	4		PASS	11	4	8.64	Normal	Normal	FACL1		long-chain acyl-CoA synthetase	ATP-binding domain (bp. 1447..1846)
L09729_s_at	L09729_s_at	L09729	fail	4		PASS	11	4	8.36	Normal	Normal			mitochondrial citrate transport protein	
SLC20A3_m	X96924_m	X96924	fail	4		PASS	11	4	8.18	Normal	Normal				KIAA0233 gene product
K233	D87071_at	D87071	fail	4		PASS	11	4	7.45	Normal	Normal	KIAA0233			
E_23773	U90904_at	U90904	fail	4		PASS	11	4	7.00	Normal	Normal			S_10-methylethyltetrahydrofolate synthetase	
MTHFD	L38928_at	L38928	fail	4		PASS	11	4	6.73	Normal	Normal			E74-like factor 4 (eis domain transcription factor)	E74-like factor 4 (eis domain transcription factor)
MEF	U32645_at	U32645	fail	4		PASS	11	4	6.27	Normal	Normal	ELF4		ornithine aminotransferase (gyrate atrophy)	ornithine aminotransferase (gyrate atrophy)
OAT	M29927_at	M29927	fail	4		PASS	11	4	6.00	Normal	Normal	OAT	10q26	MpV17 transgene, murine homolog, glomerulosclerosis	MpV17 transgene, murine homolog, glomerulosclerosis
MPV17	X76538_at	X76538	fail	4		PASS	11	4	5.82	Normal	Normal	MPV17	2p23-p21	funarate hydratase	funarate hydratase
FH	U9309_at	U9309	fail	4		PASS	11	4	5.73	Normal	Normal	FH	1q42.1	guanylate binding protein 1, interferon-inducible, 67KD	guanylate binding protein 1, interferon-inducible, 67KD
GBP1	M55542_at	M55542	fail	4		PASS	11	4	5.64	Normal	Normal	GBP1		ADP-ribosylation factor 6	ADP-ribosylation factor 6
ARF6	M57763_at	M57763	fail	3		PASS	11	3	7.64	Normal	Normal	ARF6			



# Table 1

GUBP	U78524_at	U78524	fail	3	PASS	11	3	6.00	Normal	Normal	DDXBP1	15q	DEAD/H (Asp-Glu-Ala-Asp/His) box binding protein 1	DEAD/H (Asp-Glu-Ala-Asp/His) box binding protein 1
E_23828	U79285_at	U79285	fail	3	PASS	11	3	5.73	Normal	Normal		10q23	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)
PTEN	U92436_at	U92436	fail	3	PASS	11	3	5.00	Normal	Normal	PTEN		phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)
SLBP	U75679_at	U75679	fail	3	PASS	11	3	4.91	Normal	Normal	SLBP		histone stem-loop binding protein	histone stem-loop binding protein
AFFX-HSAC	AFFX-HSAC	AFFX-HSAC	fail	1	PASS	11	1	7.27	Normal	Normal			FLT3/FLK2 ligand	FLT3/FLK2 ligand
U04806 s at	U04806 s at	U04806	fail	4	PASS	10	4	8.90	Normal	Normal			thyroid receptor interactor 7	thyroid receptor interactor 7
TRIP7	L40357_at	L40357	fail	4	PASS	10	4	7.60	Normal	Normal	TRIP7		thyroid receptor interactor 7	thyroid receptor interactor 7
STAT1	M97936_at	M97936	fail	4	PASS	10	4	7.50	Normal	Normal			lymphoid-restricted membrane protein	lymphoid-restricted membrane protein
LRMP	U10485_at	U10485	fail	4	PASS	10	4	7.00	Normal	Normal	LRMP		lymphoid-restricted membrane protein	lymphoid-restricted membrane protein
LAP18 ma1	M31303 ma	M31303	fail	4	PASS	10	4	6.60	Normal	Normal	Op18		oncogene protein 18	oncogene protein 18
DIFF48	U49187_at	U49187	fail	4	PASS	10	4	6.50	Normal	Normal	Diff48		small nuclear ribonucleoprotein D3	small nuclear ribonucleoprotein D3
SNRPD3	U15009_at	U15009	fail	4	PASS	10	4	6.40	Normal	Normal	SNRPD3		small nuclear ribonucleoprotein D3	small nuclear ribonucleoprotein D3
XG2153 s at	XG2153 s at	XG2153	fail	4	PASS	10	4	6.30	Normal	Normal			P11.1 protein	P11.1 protein
CTR2	U83461_at	U83461	fail	4	PASS	10	4	6.20	Normal	Normal	SLC31A2	9q31-q32	solute carrier family 31 (copper transporters), member 2	solute carrier family 31 (copper transporters), member 2
GPCR	L42324_at	L42324	fail	4	PASS	10	4	6.10	Normal	Normal	GPCR		G protein-linked receptor	G protein-linked receptor
EIF5	U49436_at	U49436	fail	4	PASS	10	4	6.00	Normal	Normal	EIF5		eukaryotic translation initiation factor 5	eukaryotic translation initiation factor 5
K100 EL	D43947_at	D43947	fail	4	PASS	10	4	5.90	Normal	Normal	KIAA0100		KIAA0100 gene product	KIAA0100 gene product
K274 HYON	D87464_at	D87464	fail	4	PASS	10	4	5.90	Normal	Normal	KIAA0274		glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)
GOT2	M22632_at	M22632	fail	4	PASS	10	4	5.90	Normal	Normal	GOT2	16q21	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)
DGLUOK	U41668_at	U41668	fail	4	PASS	10	4	5.90	Normal	Normal	DGLUOK		deoxyguanosine kinase	deoxyguanosine kinase
IRRCF	U18321_at	U18321	fail	4	PASS	10	4	5.80	Normal	Normal	DAP3	1q21	Death associated protein 3	Death associated protein 3
HZF1	X78924_at	X78924	fail	4	PASS	10	4	5.80	Normal	Normal	HZF1		zinc finger protein	zinc finger protein
D29640 s at	D29640 s at	D29640	fail	4	PASS	10	4	5.70	Normal	Normal	SAR1	15	rasGAP-like with IQ motifs	rasGAP-like with IQ motifs
SNRPA1	X13482_at	X13482	fail	4	PASS	10	4	5.60	Normal	Normal	SNRPA1		small nuclear ribonucleoprotein A'	small nuclear ribonucleoprotein A'
U47686 s at	U47686 s at	U47686	fail	4	PASS	10	4	5.10	Normal	Normal			signal transducer and activator of transcription Stat3B	signal transducer and activator of transcription Stat3B
K267_NAHE	D87743_at	D87743	fail	4	PASS	10	4	4.80	Normal	Normal	KIAA0267		Similar to Human Na+/H+ exchanger 2 (A57644)	Similar to Human Na+/H+ exchanger 2 (A57644)
RPP38	U77664_at	U77664	fail	4	PASS	10	4	4.70	Normal	Normal	RPP38		RNaseP protein P38	RNaseP protein P38
L38593 s at	L38593 s at	L38593	fail	3	PASS	10	3	6.50	Normal	Normal	NRAIP1		integral membrane protein	integral membrane protein
TBI	M74089_at	M74089	fail	3	PASS	10	3	5.50	Normal	Normal	TBI		cholinesterase-related cell division controller	cholinesterase-related cell division controller
CHED	M80629_at	M80629	fail	3	PASS	10	3	5.30	Normal	Normal	CDC2L		cholinesterase-related cell division controller	cholinesterase-related cell division controller
RCFN	U03644_at	U03644	fail	3	PASS	10	3	5.30	Normal	Normal	CIR		CBF1 interacting corepressor	CBF1 interacting corepressor
CCNG2	U47414_at	U47414	fail	3	PASS	10	3	5.30	Normal	Normal	CCNG2		cyclin G2	cyclin G2
E_23721	U79291_at	U79291	fail	3	PASS	10	3	5.00	Normal	Normal				

LIVP	L13800 at	L13800	fail	3		PASS	10	3	4.90	Normal	Normal	PXMP3	8q21.1	peroxisomal membrane protein 3 (35kD, Zellweger syndrome) 160 kDa subunit
PXMP3	M86852 at	M86852	fail	3		PASS	10	3	4.80	Normal	Normal			
CPSPF	U37012 at	U37012	fail	4		PASS	9	4	8.00	Normal	Normal			
CD9	M38690 at	M38690	fail	4		PASS	9	4	7.33	Normal	Normal	CD9	12p13	CD9 antigen (p24)
CASM	AF000177 at	AF000177	fail	4		PASS	9	4	7.11	Normal	Normal	CaSm		Sm-like protein; encodes Sm motifs; overexpressed in pancreatic cancer
K138 THH	D50928 at	D50928	fail	4		PASS	9	4	7.00	Normal	Normal	KIAA0138		KIAA0138 gene product
PHBLN1	U03891 at	U03891	fail	4		PASS	9	4	5.89	Normal	Normal	DJ742C19.2	22q12.3-q13.1	phorbol (similar to apolipoprotein B mRNA editing protein)
HLA-DPB1	M81664 at	M81664	fail	4		PASS	9	4	5.67	Normal	Normal	HLA-DPB1		Similar to a C.elegans protein in cosmid C14H10
K251_COSC	D87438 at	D87438	fail	4		PASS	9	4	5.44	Normal	Normal	KIAA0251		
SORD	L29008 at	L29008	fail	4		PASS	9	4	5.33	Normal	Normal	SORD	15q15-q21.1	sorbitol dehydrogenase
K92 MYH6	D42054 at	D42054	fail	4		PASS	9	4	5.22	Normal	Normal	KIAA0092	7	KIAA0092 gene product
RECA	L07493 at	L07493	fail	4		PASS	9	4	4.89	Normal	Normal	RPA3		replication protein A3 (14kD)
SCP2	U11313 at	U11313	fail	4		PASS	9	4	4.89	Normal	Normal	SCP2	1pter-p21	sterol carrier protein 2
YAF2	U72209 at	U72209	fail	4		PASS	9	4	4.78	Normal	Normal	YAF2		YY1-associated factor 2
PPP2R1B	M65254 at	M65254	fail	4		PASS	9	4	4.56	Normal	Normal	PPP2R1B	11q23	protein phosphatase-2A (formerly protein phosphatase 2 (PR 65), 2A), regulatory subunit A (PR 65), beta isoform
CD94	U30610 at	U30610	fail	3		PASS	9	3	8.44	Normal	Normal	KLRD1	12p13	killer cell lectin-like receptor
SNRPB2	M15841 at	M15841	fail	3		PASS	9	3	7.44	Normal	Normal	SNRPB2		subfamily D, member 1
CLC	L01664 at	L01664	fail	3		PASS	9	3	7.22	Normal	Normal	CLC	19q13.1	small nuclear ribonucleoprotein polypeptide B*
AFEX-HUM6	AFEX-HUM6 at	AFEX-HUM6	fail	3		PASS	9	3	7.11	Normal	Normal			Charot-Leyden crystal protein
SNX1	U53225 at	U53225	fail	3		PASS	9	3	6.67	Normal	Normal	SNX1		sorting nexin 1
FKBP5	U42031 at	U42031	fail	3		PASS	9	3	6.56	Normal	Normal	FKBP5		FK506-binding protein 5
S72024 s at	S72024 s at	S72024	fail	3		PASS	9	3	6.44	Normal	Normal	cit-5A		eukaryotic initiation factor 5A
SMARCC1	U66615 at	U66615	fail	3		PASS	9	3	5.67	Normal	Normal	SMARCC1	3p23-p21	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1
L05624 s at	L05624 s at	L05624	fail	3		PASS	9	3	5.56	Normal	Normal			MAP kinase kinase
TPP2	M71047 at	M71047	fail	3		PASS	9	3	5.56	Normal	Normal	TPP2	13q32-q33	tripeptidyl peptidase II
PLK	U01038 at	U01038	fail	3		PASS	9	3	5.56	Normal	Normal			signal transducer and activator of transcription 6, interleukin-4 induced
STAT6	U16031 at	U16031	fail	3		PASS	9	3	5.56	Normal	Normal	STAT6	12q13	signal transducer and activator of transcription 6, interleukin-4 induced
NUP88	Y08612 at	Y08612	fail	3		PASS	9	3	5.44	Normal	Normal	NUP88	17p13	nucleoporin 88kD
S79219_s at	S79219_s at	S79219	fail	3		PASS	9	3	5.22	Normal	Normal	PCCA	13q32	propionyl Coenzyme A carboxylase, alpha polypeptide

C2F	U72514_at	U72514	fail	3	PASS	9	3	5.00	Normal	Normal	C2F	C2F	similar to EST with GenBank Accession Number R64505; similar to S. cerevisiae hypothetical protein L9470.5 encoded by GenBank Accession Number S51431, and to S. pombe hypothetical 34.9 KD protein encoded by GenBank Accession Number Z68198; see corresponding genomic sequence in GenBank Accession Number U72506
E_23733	U79274_at	U79274	fail	3	PASS	9	3	5.00	Normal	Normal			deoxycytidine kinase
DCK	M60527_at	M60527	fail	3	PASS	9	3	4.67	Normal	Normal	DCK	4q13.3-q21.1	
AFEX-BioB	AFEX-BioB	AFEX-BioB	fail	0	PASS	9	0	17.44	Normal	Normal			
RES24A	AB000464_at	AB000464	fail	4	PASS	8	4	8.50	Normal	Normal			
SSRP1	M86737_at	M86737	fail	4	PASS	8	4	7.75	Normal	Normal	SSRP1	11q12	structure specific recognition protein 1
BAT3	M33521_at	M33521	fail	4	PASS	8	4	2.50	Normal	Normal	D6S52E	6p21.3	HLA-B associated transcript-3
PNOC	U48263_at	U48263	fail	4	PASS	8	4	7.00	Normal	Normal	OFQ		pre-pro-orphanin FQ
ERCC1	M13194_at	M13194	fail	4	PASS	8	4	6.63	Normal	Normal	ERCC1	19q13.2-q13.3	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)
TRNAGUTR	U30888_at	U30888	fail	4	PASS	8	4	6.38	Normal	Normal	USP14		tRNA-Guanine Transglycosylase
L24774_s_at	L24774_s_at	L24774	fail	4	PASS	8	4	5.88	Normal	Normal	DCI	16p13.3	dodecenoyl-Coenzyme A delta isomerase (3.2 trans-enoyl-Coenzyme A isomerase)
HG3319-HTG9	HG3319-HTG9	HG3319-HTG9	fail	4	PASS	8	4	5.63	Normal	Normal	NEU	6 or 10pter-q23	neuraminidase
ZNF139	U09848_at	U09848	fail	4	PASS	8	4	5.00	Normal	Normal	ZNF139		zinc finger protein 139 (clone pTZ-37)
ZFX	X59739_at	X59739	fail	4	PASS	8	4	5.00	Normal	Normal	ZFX	Xp22.1-p21.3	zinc finger protein, X-linked
S80267_s_at	S80267_s_at	S80267	fail	4	PASS	8	4	4.88	Normal	Normal	p72syk		This sequence comes from Fig. 3.
DARS	J05032_at	J05032	fail	4	PASS	8	4	4.63	Normal	Normal	DARS		aspartyl-RNA synthetase
U18271_cds	U18271_cds	U18271	fail	4	PASS	8	4	4.63	Normal	Normal	TMPO		thymopoeitin beta
K128_HCDC	D50918_at	D50918	fail	3	PASS	8	3	7.13	Normal	Normal	KIAA0128		The KIAA0128 gene is related to cdc10.
TDRAA	HG3378-HTG	HG3378-HTG	fail	3	PASS	8	3	6.25	Normal	Normal	LAMB2		lamin B2
LAMB2	M94362_at	M94362	fail	3	PASS	8	3	6.00	Normal	Normal	LAMB2		GAP SH3 binding protein
SH3BP2	U32519_at	U32519	fail	3	PASS	8	3	5.50	Normal	Normal			
MURK1	D85433_at	D85433	fail	3	PASS	8	3	5.38	Normal	Normal	ITGAE		integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide)
ITGAE	L25851_at	L25851	fail	3	PASS	8	3	5.25	Normal	Normal			integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide)
SPLREGSUP	U08377_at	U08377	fail	3	PASS	8	3	5.25	Normal	Normal	SFRS8		splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot, Drosophila homolog)

# Table 1

STX16C	AF008937	at	AF008937	fail	3		PASS	8	3	5.00	Normal	Normal	STX16		synixin 16		synixin 16		The long form does not bind to the integrin beta 3 subunit cytoplasmic domain
ANX3B	U37139	at	U37139	fail	3		PASS	8	3	4.88	Normal	Normal			beta 3-endonexin long form				
K33	D26067	at	D26067	fail	3		PASS	8	3	4.75	Normal	Normal	KIAA0033						
AHR	L19872	at	L19872	fail	3		PASS	8	3	4.75	Normal	Normal	AHR	7p15	aryl hydrocarbon receptor		aryl hydrocarbon receptor		
MEST	D78611	at	D78611	fail	3		PASS	8	3	4.38	Normal	Normal	MEST	7q32	mesoderm specific transcript (mouse) homolog		mesoderm specific transcript (mouse) homolog		
PIGH	L19783	at	L19783	fail	3		PASS	8	3	4.38	Normal	Normal	PIGH	14q11-q24	phosphatidylinositol glycan, class H		phosphatidylinositol glycan, class H		
M34338	s a	M34338	s a	M34338	fail	2	PASS	8	2	7.50	Normal	Normal	SRM	1p36-p22	spemidine synthase		spemidine synthase		
WWP1	U96113	at	U96113	fail	2		PASS	8	2	5.88	Normal	Normal	WWP1				WWP1		Nedd4-like ubiquitin-protein ligase; WW domain-containing protein
RH17599	L06175	at	L06175	fail	2		PASS	8	2	5.75	Normal	Normal	P5-1						occurs in MHC class I region; ORF
ITBA1	X92475	at	X92475	fail	2		PASS	8	2	5.75	Normal	Normal	ITBA1	Xq28	ITBA1 protein		ITBA1 gene		
CL1042	X70649	at	X70649	fail	2		PASS	8	2	5.38	Normal	Normal	DDX1	2p24	member of DEAD box protein family		DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1		
HG3417-HT	HG3417-HT	M88282	M88282	fail	2		PASS	8	2	5.25	Normal	Normal					tactile protein		T cell surface antigen, increased during activation
TACT	M88282	at	M88282	fail	2		PASS	8	2	5.25	Normal	Normal							
ZFP2	U71598	at	U71598	fail	2		PASS	8	2	5.25	Normal	Normal	zif2		zinc finger protein zip2				
K116 75KD	D29958	at	D29958	fail	2		PASS	8	2	5.13	Normal	Normal	KIAA0116				inogen 38		proprotein
IMOG38	Z68747	at	Z68747	fail	2		PASS	8	2	5.13	Normal	Normal					ANA		
BTG3	D64110	at	D64110	fail	2		PASS	8	2	5.00	Normal	Normal							
RATC10	HG1879-HT	HG1879-HT	HG1879-HT	fail	2		PASS	8	2	5.00	Normal	Normal							
GCF	M29204	at	M29204	fail	2		PASS	8	2	5.00	Normal	Normal	TCF9	2p11.2-p11.1	transcription factor 9 (binds GC-rich sequences)		transcription factor 9 (binds GC-rich sequences)		
HG3546-HT	HG3546-HT	HG3546-HT	HG3546-HT	fail	2		PASS	8	2	4.88	Normal	Normal							
ATF1	X55544	at	X55544	fail	2		PASS	8	2	4.75	Normal	Normal	ATF1	12q13	TREB protein		activating transcription factor 1		
UNKP	U50950	at	U50950	fail	2		PASS	8	2	4.13	Normal	Normal							
ALDOC	X05196	at	X05196	fail	1		PASS	8	1	7.00	Normal	Normal	ALDOC	17cen-q12	aldolase C		aldolase C, fructose-bisphosphate		
SEC23B	X97065	at	X97065	fail	1		PASS	8	1	6.13	Normal	Normal	sec23		Sec23 protein		COP11 component; isoform B		
GT2B	M76766	at	M76766	fail	1		PASS	8	1	5.88	Normal	Normal	GT2B	1p22-p21	general transcription factor IIB		general transcription factor IIB		
RPP30	U77665	at	U77665	fail	1		PASS	8	1	5.63	Normal	Normal	RPP30		RNAseP protein P30		succinate-CoA ligase, GDP-forming, alpha subunit		
COASYNT	Z68204	at	Z68204	fail	1		PASS	8	1	5.50	Normal	Normal	SUCLG1		succinyl coenzyme A synthetase		DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3		
DDX3	U50553	at	U50553	fail	1		PASS	8	1	5.13	Normal	Normal	DDX3	Xp11.3-p11.23	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3		CDIC antigen, c polypeptide		
SFRS2	HG1088-HT	HG1088-HT	HG1088-HT	fail	1		PASS	8	1	4.75	Normal	Normal					CDIC antigen, c polypeptide		
CDIC	M28827	at	M28827	fail	1		PASS	8	1	4.75	Normal	Normal	CDIC	1q22-q23	basic transcription factor 62kD subunit		casein kinase 1, alpha 1		
BT2F	M95809	at	M95809	fail	1		PASS	8	1	4.75	Normal	Normal	BT2F		Translin associated protein X		RAB33A, member RAS oncogene family		
TSNAX	X95073	at	X95073	fail	1		PASS	8	1	4.75	Normal	Normal	TRAX		casein kinase 1, alpha 1		RAB33A, member RAS oncogene family		
CSNK1A1	L37042	at	L37042	fail	4		PASS	7	4	8.00	Normal	Normal	CSNK1A1	13q13	phospholipase c delta 1		AE-binding protein 1		
PLCD1	U09117	at	U09117	fail	4		PASS	7	4	7.57	Normal	Normal		X	RAB33A, member RAS oncogene family		homolog of fission yeast Skb1		
S10	D14889	at	D14889	fail	4		PASS	7	4	5.71	Normal	Normal	RAB33A		AE-binding protein 1				
AEBP1	D86479	at	D86479	fail	4		PASS	7	4	5.71	Normal	Normal	AEBP1	7	AE-binding protein 1				
SKB1	AF015913	at	AF015913	fail	4		PASS	7	4	5.57	Normal	Normal	SKB1Hs		homolog of fission yeast Skb1				

# Table 2

K03498_xpt1	K03498_xpt1	K03498	fail	4		PASS	7	4	5.57	Normal	Normal		pol protein	env ORF (bases 110-8290) first start codon at 191: putative
SL1	L39059 at	L39059	fail	4		PASS	7	4	5.43	Normal	Normal		transcription factor SL1	phosphatidylinositol glycan, class F
PIGF	D13435 at	D13435	fail	4		PASS	7	4	5.29	Normal	Normal		PIGF	phosphatidylinositol glycan, class F
TCF4	M74719 at	M74719	fail	4		PASS	7	4	5.14	Normal	Normal		TCF4	transcription factor 4
GOLGA1	U51587 at	U51587	fail	4		PASS	7	4	5.14	Normal	Normal		GOLGA1	golgi autoantigen, golgin subfamily a, 1
X75091_s at	X75091_s at	X75091	fail	4		PASS	7	4	5.00	Normal	Normal		PHAPII (putative HLA DR Associated Protein II)	
POLR3	U93867 at	U93867	fail	4		PASS	7	4	4.71	Normal	Normal		RNA polymerase III subunit	glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD)
GLCLC	M90656 at	M90656	fail	4		PASS	7	4	4.43	Normal	Normal		GLCLC	glutamate-cysteine ligase
PTPRE	HG620-HT62	HG620-HT	fail	3		PASS	7	3	8.00	Normal	Normal			
OBGRP	Y12670 at	Y12670	fail	3		PASS	7	3	8.00	Normal	Normal		OB-RGRP	leptin receptor gene-related protein
DRNM23	U29656 at	U29656	fail	3		PASS	7	3	7.29	Normal	Normal		NME3	non-metastatic cells 3, protein expressed in
OMD	AB000114 a	AB000114	fail	3		PASS	7	3	6.86	Normal	Normal		OMD	osteomodulin
RY1	X76302 at	X76302	fail	3		PASS	7	3	6.86	Normal	Normal		RY-1	nucleic acid binding protein
K12_TOLL	D13637 at	D13637	fail	3		PASS	7	3	6.57	Normal	Normal		TLR1	toll-like receptor 1
CSNK2A1	M55265 at	M55265	fail	3		PASS	7	3	5.86	Normal	Normal		CSNK2A1	casein kinase 2, alpha 1 polypeptide
DOC2	U53446 at	U53446	fail	3		PASS	7	3	5.86	Normal	Normal		DAB2	disabled (Drosophila) homolog 2 (mitogen-responsive phosphoprotein)
SMARCD1	U66617 at	U66617	fail	3		PASS	7	3	5.71	Normal	Normal		SMARCD1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1
ZNF131	U09410 at	U09410	fail	3		PASS	7	3	5.43	Normal	Normal		ZNF131	zinc finger protein 131 (clone pHZ-10)
GLIPR	U16307 at	U16307	fail	3		PASS	7	3	5.43	Normal	Normal		GLIPR	glioma pathogenesis-related protein
E2F5	U31556 at	U31556	fail	3		PASS	7	3	5.43	Normal	Normal		E2F-5	transcription factor
BARD1	U76638 at	U76638	fail	3		PASS	7	3	4.29	Normal	Normal		BARD1	BRCA1 associated RING domain 1
U40763 s at	U40763 s at	U40763	fail	3		PASS	7	3	4.14	Normal	Normal		CYP	Clk-associating RS-cyclophilin
ARH9	L25081 at	L25081	fail	2		PASS	7	2	8.86	Normal	Normal		ARHC	ras homolog gene family, member C
HSN	U03057 at	U03057	fail	2		PASS	7	2	8.86	Normal	Normal		SNL	singed (Drosophila)-like (sea urchin) fascin homolog like
TARS	M63180 at	M63180	fail	2		PASS	7	2	5.57	Normal	Normal		TARS	threonyl-RNA synthetase
K182	D80004 at	D80004	fail	2		PASS	7	2	5.43	Normal	Normal		KIAA0182	
TFAP3B	U91931 at	U91931	fail	2		PASS	7	2	5.43	Normal	Normal		ADTB3	Beta-3A-adaptin
CTIP	U72066 at	U72066	fail	2		PASS	7	2	5.14	Normal	Normal		RBBP8	retinoblastoma-binding protein 8
CD72	M54992 at	M54992	fail	2		PASS	7	2	5.00	Normal	Normal		CD72	CD72 antigen
PDE6B	S41458 at	S41458	fail	2		PASS	7	2	4.86	Normal	Normal		PDE6B	phosphodiesterase 6B, cGMP-specific, rod, beta (congenital stationary night blindness 3, autosomal dominant)

Gene	UT3737 at	UT3737	fail	2		PASS	7	2	4.86	Normal	Normal	GTBP	2p16	GT mismatch-binding protein	GT mismatch-binding protein
UGT3732 s at	UGT3732 s at	UGT3732	fail	2		PASS	7	2	4.57	Normal	Normal	Pde7A2		cAMP phosphodiesterase	
GBE1	L07936_at	L07936	fail	2		PASS	7	2	4.43	Normal	Normal	GBE1	3p21	glucan (1,4-alpha), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV)	glucan (1,4-alpha), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV)
CDR2	M63256_at	M63256	fail	2		PASS	7	2	4.43	Normal	Normal	CDR2	16p13.1-p12	major Yo paraneoplastic antigen	cerebellar degeneration-related protein (62KD)
RPIH	U90437 at	U90437	fail	2		PASS	7	2	4.29	Normal	Normal			heterogeneous	linRNP protein; linRNA binding protein
HNRPA0	U23803_at	U23803	fail	1		PASS	7	1	8.71	Normal	Normal			ribonucleoprotein A0	
ICRF	Z69915 at	Z69915	fail	1		PASS	7	1	6.00	Normal	Normal			signal sequence receptor, alpha (translocon-associated protein alpha)	signal sequence receptor, alpha (translocon-associated protein alpha)
SSR1	Z12830_at	Z12830	fail	1		PASS	7	1	5.86	Normal	Normal	SSR1		Ral guanine nucleotide dissociation stimulator	the C-terminal non-catalytic domain of the Ral GDS interacts with Ras
RALGDS	U14417_at	U14417	fail	1		PASS	7	1	5.71	Normal	Normal			SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2
SMARCC2	U66616_at	U66616	fail	1		PASS	7	1	5.71	Normal	Normal	SMARCC2	12q13-q14	propionyl Coenzyme A carboxylase, beta polypeptide	propionyl Coenzyme A carboxylase, beta polypeptide
PCCB	S67325_at	S67325	fail	1		PASS	7	1	5.29	Normal	Normal	PCCB	3q21-q22	glt6 protein	glt6 protein
GLP2	U50839 at	U50839	fail	1		PASS	7	1	5.00	Normal	Normal	GLP2		cullin 2	cullin 2
CUL2	U83410 at	U83410	fail	1		PASS	7	1	5.00	Normal	Normal	CUL2		CCAAT/enhancer binding protein (C/EBP), gamma	CCAAT/enhancer binding protein (C/EBP), gamma
CEBPG	U20240_at	U20240	fail	1		PASS	7	1	4.86	Normal	Normal	CEBPG		RAB9, member RAS oncogene family	RAB9, member RAS oncogene family
RAB9	U44103_at	U44103	fail	1		PASS	7	1	4.86	Normal	Normal	RAB9		ubiquitin specific protease 8	ubiquitin specific protease 8
K55 TRE	D29956 at	D29956	fail	1		PASS	7	1	4.43	Normal	Normal	USP8		cysteine-rich protein 2	cysteine-rich protein 2
CRIP2	D42123 at	D42123	PASS	9	25.56	fail	5	9		Disease	Disease	CRIP2	14q32.3	KIAA0014 gene product	KIAA0014 gene product
K14	D25216 at	D25216	PASS	9	31.67	fail	5	9		Disease	Disease	KIAA0014		leukocyte tyrosine kinase	leukocyte tyrosine kinase
LTK	D16105 at	D16105	PASS	9	23.78	fail	3	9		Disease	Disease	LTK	15	KIAA0060 gene product	KIAA0060 gene product
K60 GNPTA	D31766 at	D31766	PASS	8	14.50	fail	6	8		Disease	Disease	KIAA0060		cyclin-dependent kinase 2	cyclin-dependent kinase 2
CDK2	M68520 at	M68520	PASS	8	7.63	fail	6	8		Disease	Disease	CDK2	12q13	interleukin 11 receptor, alpha	interleukin 11 receptor, alpha
IL11RA	U32324 at	U32324	PASS	8	9.75	fail	6	8		Disease	Disease	IL11RA	9p13	acid phosphatase	acid phosphatase
ACP2 mal	X15525 ma	X15525	PASS	8	8.75	fail	6	8		Disease	Disease	ACP2		homologous to mouse gene PC326; GenBank Accession Number M95564	homologous to mouse gene PC326; GenBank Accession Number M95564
H326	U06631 at	U06631	PASS	8	23.13	fail	5	8		Disease	Disease	H326		KIAA0170 gene product	KIAA0170 gene product
TEB4	AF009301 at	AF009301	PASS	8	9.88	fail	5	8		Disease	Disease	TEB4		protein kinase, cAMP-dependent, catalytic, gamma	protein kinase, cAMP-dependent, catalytic, gamma
K170 CALT	D79992 at	D79992	PASS	8	6.88	fail	5	8		Disease	Disease	KIAA0170		plectin 1, intermediate filament binding protein, 500KD	plectin 1, intermediate filament binding protein, 500KD
PRKACG	M34182 at	M34182	PASS	8	41.00	fail	5	8		Disease	Disease	PRKACG	9q13	protein, Swiss-Prot Accession Number P19333	protein, Swiss-Prot Accession Number P19333
PLEC1	U53204 at	U53204	PASS	8	40.38	fail	4	8		Disease	Disease	PLEC1	8q24		
E_LF113	U18009 at	U18009	PASS	8	13.00	fail	4	8		Disease	Disease				
18SRNA5	AFEX-HUM	AFEX-HUN	PASS	8	12.00	fail	3	8		Disease	Disease				
MUC3	HG2147-HTT	HG2147-H	PASS	8	60.63	fail	3	8		Disease	Disease				

MYBPC3	X73113_at	X73113	PASS	8	11.25	fail	3	8		Disease	Disease	MYBPC2	19	myosin-binding protein C, fast-type
NB	D89016_at	D89016	PASS	8	20.63	fail	2	8		Disease	Disease			myosin-binding protein C, fast-type
U47025_s_at	U47025_s_at	U47025	PASS	7	27.43	fail	6	7		Disease	Disease	Neuroblastoma		phosphorylase, glycogen; brain
KIDNABP	D45132_at	D45132	PASS	7	5.86	fail	6	7		Disease	Disease	PYGB	20	phosphorylase, glycogen; brain
K179_HYPD	D80001_at	D80001	PASS	7	8.00	fail	6	7		Disease	Disease	KIAA0179		zinc-finger DNA-binding protein
K213	D86968_at	D86968	PASS	7	4.14	fail	6	7		Disease	Disease	KIAA0213		similar to hypothetical protein D4478 of Scerevisiae.
HG2175-HT2	HG2175-HT2	HG2175-HT2	PASS	7	5.43	fail	6	7		Disease	Disease			Similar to Mouse TfR1-associated transactivator factor p17(GB, RO:MMU11548): Containing protein kinase motif
INPL1	L36818_at	L36818	PASS	7	21.71	fail	6	7		Disease	Disease			
GSI	M86934_at	M86934	PASS	7	8.14	fail	6	7		Disease	Disease	GSI		Gene from Xp22.3 which escapes X-inactivation. Function unknown.
MFAP1	U04209_at	U04209	PASS	7	6.00	fail	6	7		Disease	Disease			
IFNRG7A	U53830_at	U53830	PASS	7	15.29	fail	6	7		Disease	Disease	IRF7	11	interferon regulatory factor 7
GABRA1	X14766_at	X14766	PASS	7	8.71	fail	6	7		Disease	Disease	GABRA1	5q34-q35	gamma-aminobutyric acid (GABA) A receptor, alpha 1
CSRP1	M76378_at	M76378	PASS	7	23.29	fail	5	7		Disease	Disease	CSRP1	1q32	cysteine and glycine-rich protein 1
K146	D63480_at	D63480	PASS	7	6.14	fail	5	7		Disease	Disease	KIAA0146		The KIAA0146 gene product is novel.
GLGF2	HG4704-HT2	HG4704-HT2	PASS	7	6.14	fail	5	7		Disease	Disease			
TAL1	M63589_at	M63589	PASS	7	13.00	fail	5	7		Disease	Disease	TAL1	1p32	T-cell acute lymphocytic leukemia 1
SLAHBP1	U51586_at	U51586	PASS	7	8.29	fail	5	7		Disease	Disease	SLAHBP1		T-cell acute lymphocytic leukemia 1
ENO2_ma1	X51956_ma1	X51956	PASS	7	9.43	fail	5	7		Disease	Disease	ENO2	12p13	enolase 2, (gamma, neuronal)
K27	D25217_at	D25217	PASS	7	16.29	fail	4	7		Disease	Disease	KIAA0027		
EBI3	L08187_at	L08187	PASS	7	13.86	fail	4	7		Disease	Disease	EBI3		cytokine receptor
RETROTP	Z48633_at	Z48633	PASS	7	12.14	fail	4	7		Disease	Disease			
SP2	D28588_at	D28588	PASS	6	6.83	fail	6	6		Disease	Disease	SP2		Sp2 transcription factor
K263_HYPY	D87452_at	D87452	PASS	6	13.33	fail	6	6		Disease	Disease	KIAA0263		KIAA0263 gene product
HEPG2	K03195_at	K03195	PASS	6	9.50	fail	6	6		Disease	Disease	SGLT1		glucose transporter glycoprotein
IDS	L40586_at	L40586	PASS	6	6.67	fail	6	6		Disease	Disease	IDS	Xq27.3-q28	iduronate 2-sulfatase (Hunter syndrome)
FOSB	L49169_at	L49169	PASS	6	10.67	fail	6	6		Disease	Disease	GOS3		GOS3 is human homolog of mouse FOSB gene
MYOIC	U14391_at	U14391	PASS	6	9.00	fail	6	6		Disease	Disease	MYOIC	15q21-q22	myosin IC
HCCS	U36787_at	U36787	PASS	6	7.00	fail	6	6		Disease	Disease			putative
HA2	X90761_at	X90761	PASS	6	8.67	fail	6	6		Disease	Disease	KRT42	17q12-q21	keratin, hair, acidic,2
X92493_s_at	X92493_s_at	X92493	PASS	6	5.00	fail	6	6		Disease	Disease	PIPSK1B	9q13	phosphatidylinositol-4-phosphate 5-phosphate 5-kinase, type I, beta
XPA	D14533_at	D14533	PASS	6	4.50	fail	5	6		Disease	Disease	XPA	9	xeroderma pigmentosum, complementation group A
K76	D38548_at	D38548	PASS	6	16.33	fail	5	6		Disease	Disease	KIAA0076		KIAA0076 gene product
K268_C219R	D87742_at	D87742	PASS	6	5.17	fail	5	6		Disease	Disease	KIAA0268		Similar to Human C219-reactive peptide (L34688)
DAO	HG2280-HT2	HG2280-HT2	PASS	6	15.50	fail	5	6		Disease	Disease			

H2A1B	L19778 at M64571	PASS	6	5.00	fail	5	6	Disease	Disease	H2A1B	microtubule-associated protein 4	H2A histone family, member P
MAP4	M64571 at M79462	PASS	6	11.83	fail	5	6	Disease	Disease	MAP4	promyelocytic leukemia	promyelocytic leukemia
PML	M79462 at S78798	PASS	6	12.00	fail	5	6	Disease	Disease	PML	1-phosphatidylinositol-4-phosphate 5-kinase isoform C	Method: conceptual translation with partial peptide sequencing. This sequence comes from Fig. 2; PtdIns4P 5-kinase isoform C
S78798_s_at	S78798_s_at	PASS	6	6.50	fail	5	6	Disease	Disease			
HSD17B3	U05659 at U11090	PASS	6	18.17	fail	5	6	Disease	Disease	HSD17B3	hydroxysteroid (17-beta) dehydrogenase 3	hydroxysteroid (17-beta) dehydrogenase 3
ASMT	U11090 at U18259	PASS	6	11.50	fail	5	6	Disease	Disease	ASMT	acetylserotonin N-methyltransferase	acetylserotonin N-methyltransferase
MHC2TA	U18259 at U22431_s_at	PASS	6	5.00	fail	5	6	Disease	Disease	MHC2TA	MHC class II transactivator	MHC class II transactivator
U22431_s_at	U22431_s_at	PASS	6	6.83	fail	5	6	Disease	Disease	HIF1A	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
SNAP	U39412 at U43189_s_at	PASS	6	16.50	fail	5	6	Disease	Disease	NAP	N-ethylmaleimide-sensitive factor attachment protein, alpha	N-ethylmaleimide-sensitive factor attachment protein, alpha
U43189_s_at	U43189_s_at	PASS	6	7.17	fail	5	6	Disease	Disease	NERF-1b	NERF-1b	Ets transcription factor
CHM	U84720 at X53586	PASS	6	11.83	fail	5	6	Disease	Disease	RAE1	homolog of yeast Rae1 (Bharathi)	mRNA-associated protein of 41 kDa (Kraemer)
ITGA6	X53586 at D83597	PASS	6	8.83	fail	5	6	Disease	Disease	ITGA6	integrin, alpha 6	integrin, alpha 6
LY64	D83597 at L13744	PASS	6	11.83	fail	4	6	Disease	Disease	LY64	lymphocyte antigen 64 (mouse)	lymphocyte antigen 64 (mouse)
MLLT3	L13744 at S75295	PASS	6	5.00	fail	4	6	Disease	Disease	AF-9	AF-9	homolog, radioprotective, 105kD
KPNA1	S75295 at U09366	PASS	6	5.67	fail	4	6	Disease	Disease	KPNA1	karyopherin alpha 1 (importin alpha 5)	karyopherin alpha 1 (importin alpha 5)
ZNF169	U09366 at U30894	PASS	6	7.50	fail	4	6	Disease	Disease	ZNF169	zinc finger protein 169	zinc finger protein 169
SGSH	U30894 at D14686	PASS	6	10.50	fail	4	6	Disease	Disease	SGSH	N-sulfolglucosamine sulfolglucosaminase (sulfamidase)	N-sulfolglucosamine sulfolglucosaminase (sulfamidase)
AMT	D14686 at D38122	PASS	5	12.20	fail	6	5	Disease	Disease	AMT	aminomethyltransferase (glycine cleavage system protein T)	aminomethyltransferase (glycine cleavage system protein T)
APT1LG1	D38122 at D42046	PASS	5	5.40	fail	6	5	Disease	Disease	TNFSF6	apoptosis (APO-1) antigen ligand 1	tumor necrosis factor (ligand) superfamily, member 6
K83_CHR3	D42046 at D50863	PASS	5	6.60	fail	6	5	Disease	Disease	DNA2L	DNA2 (DNA replication helicase)	DNA2 (DNA replication helicase)
TESK1	D50863 at D79994	PASS	5	8.80	fail	6	5	Disease	Disease	TESK1	testis-specific kinase 1	testis-specific kinase 1
K172_ANK3	D79994 at HG1783-HT	PASS	5	6.20	fail	6	5	Disease	Disease	KIAA0172	similar to ankryrin of Chromatium vinosum	similar to ankryrin of Chromatium vinosum
HG1783-HT	HG1783-HT	PASS	5	4.60	fail	6	5	Disease	Disease			
HOXP12	HG2810-HT	PASS	5	6.00	fail	6	5	Disease	Disease			
X104	L27476 at	PASS	5	5.20	fail	6	5	Disease	Disease	ZO-2	Friedreich ataxia region gene X104 (tight junction protein ZO-2)	Friedreich ataxia region gene X104 (tight junction protein ZO-2)



BRE	L38616_at	L38616	PASS	5	11.00	fail	6	5		Disease	Disease	BRE		brain and reproductive organ-expressed (TNFRSF1A modulator)	brain and reproductive organ-expressed (TNFRSF1A modulator)
ZNF8	M29581_at	M29581	PASS	5	8.80	fail	6	5		Disease	Disease	ZNF8	20q13		zinc finger protein 8 (clone HF.18)
U50648_s_at	U50648_s_at	U50648	PASS	5	24.60	fail	6	5		Disease	Disease	PRKR	2p22-p21	protein kinase, interferon-inducible double stranded RNA dependent	protein kinase, interferon-inducible double stranded RNA dependent
SCA2	U70323_at	U70323	PASS	5	12.20	fail	6	5		Disease	Disease	SCA2	12q24	ataxin 2	spinocerebellar ataxia 2 (olivopontocerebellar ataxia 2, autosomal dominant, ataxin 2)
ADARB1	U76421_at	U76421	PASS	5	6.20	fail	6	5		Disease	Disease	ADARB1	21q22.3	adenosine deaminase, RNA-specific, B1 (homolog of rat RED1)	adenosine deaminase, RNA-specific, B1 (homolog of rat RED1)
TSG101	U82130_at	U82130	PASS	5	7.80	fail	6	5		Disease	Disease	TSG101		tumor susceptibility protein	phosphonammonase 1
PMM1	U86070_at	U86070	PASS	5	12.60	fail	6	5		Disease	Disease	PMM1	22q13	phosphonammonase 1	thiosulfate sulfurtransferase (rhodanese)
TST	X59434_at	X59434	PASS	5	8.80	fail	6	5		Disease	Disease	TST			phosphonammonase 1
PFKP	D25328_at	D25328	PASS	5	8.60	fail	5	5		Disease	Disease	PFKP	10p15	platelet-type phosphofructokinase	phosphofructokinase, platelet
K65_ZNF111D31763_at	D31763	D31763	PASS	5	7.60	fail	5	5		Disease	Disease	KIAA0065			ha0946 protein is Kruppel-related
K188_SMP2	D80010_at	D80010	PASS	5	5.40	fail	5	5		Disease	Disease	KIAA0188			
HG2809-HT2	HG2809-HT2	HG2809-HT2	PASS	5	9.80	fail	5	5		Disease	Disease				
M11025_s_at	M11025_s_at	M11025	PASS	5	6.40	fail	5	5		Disease	Disease	ASGR2	17p	asialoglycoprotein receptor 2	asialoglycoprotein receptor 2
M19267_s_at	M19267_s_at	M19267	PASS	5	7.80	fail	5	5		Disease	Disease	TPM1	15q22.1	tropomyosin 1 (alpha)	tropomyosin 1 (alpha)
TNNC1_ma	M37984_ma	M37984	PASS	5	12.80	fail	5	5		Disease	Disease	TnC		slow twitch skeletal/cardiac muscle tropomyosin C	putative
ECGF1	S72487_at	S72487	PASS	5	10.00	fail	5	5		Disease	Disease	orf1 5' to PD-ECGF/TP			
EIF2B	U23028_at	U23028	PASS	5	8.20	fail	5	5		Disease	Disease	EIF2B5		eIF-2B epsilon	eukaryotic translation initiation factor 2B, subunit 5 (epsilon, 82kD)
CBLB	U26710_at	U26710	PASS	5	6.20	fail	5	5		Disease	Disease	CBLB	3q	Cas-Br-M (murine) ectropic retroviral transforming sequence b	Cas-Br-M (murine) ectropic retroviral transforming sequence b
ADK	U50196_at	U50196	PASS	5	5.00	fail	5	5		Disease	Disease			adenosine kinase	putative polymerase; orf similar to the integrase domain of Type A and Type B retroviruses and to class II HERVs
ERVK_cds2	U60269_cds2	U60269	PASS	5	5.80	fail	5	5		Disease	Disease				alternative initiation codon used
U68162_cds	U68162_cds	U68162	PASS	5	6.40	fail	5	5		Disease	Disease	MPL		thrombopoietin receptor	POU domain, class 2, associating factor 1
POU2AF1	Z49194_at	Z49194	PASS	5	7.20	fail	5	5		Disease	Disease	POU2AF1	11q23.1	oct-binding factor	POU domain, class 2, associating factor 1
K334	AB002332_a	AB002332	PASS	5	4.80	fail	4	5		Disease	Disease	GLOK	4q12	clock (mouse) homolog	clock (mouse) homolog
K238_PERM	D87075_at	D87075	PASS	5	6.00	fail	4	5		Disease	Disease	KIAA0238			similar to Mouse yolk sac permease like molecule 1 (U25739)
K238	D87447_at	D87447	PASS	5	9.20	fail	4	5		Disease	Disease	KIAA0258		KIAA0258 gene product	KIAA0258 gene product
K279_EGFL	D87469_at	D87469	PASS	5	5.80	fail	4	5		Disease	Disease	EGFL2	chr. 1	EGF-like domain, multiple 2	EGF-like domain, multiple 2
AMY2B	D90097_at	D90097	PASS	5	5.60	fail	4	5		Disease	Disease	AMY2B	1p21	alpha-amylase	amylase, alpha 2B; pancreatic
M34458_ma	M34458_ma	M34458	PASS	5	5.80	fail	4	5		Disease	Disease			lamin B	lamin B

M81182_s_a	M81182_s_a	M81182	PASS	5	5.00	fail	4	5		Disease	Disease	PXMP1	1p22-p21	peroxisomal membrane protein 1 (70kD, Zellweger syndrome)	peroxisomal membrane protein 1 (70kD, Zellweger syndrome)
HRC1	M91083_at	M91083	PASS	5	8.00	fail	4	5		Disease	Disease	CTORF13	11p15.5	HRAS1-related cluster-1	chromosome 11 open reading frame 13
ITGB3	S70348_at	S70348	PASS	5	7.00	fail	4	5		Disease	Disease	integrin beta 3		integrin beta 3	This sequence comes from Fig. 1a. Protein sequence is in conflict with the conceptual translation; mismatch(29(G->Gt;Q))
PTFD	U44755_at	U44755	PASS	5	9.00	fail	4	5		Disease	Disease	SNAPC2		small nuclear RNA activating complex, polypeptide 2, 45kD	small nuclear RNA activating complex, polypeptide 2, 45kD
GCDH	U69141_at	U69141	PASS	5	6.40	fail	4	5		Disease	Disease	GCDH	19p13.2	glutaryl-Coenzyme A dehydrogenase	glutaryl-Coenzyme A dehydrogenase
UNKP	D28124_at	D28124	PASS	5	16.40	fail	3	5		Disease	Disease	NBL1	1p36.3-p36.2	neuroblastoma candidate region, suppression of tumorigenicity 1	neuroblastoma candidate region, suppression of tumorigenicity 1
NCBP1P1	D59253_at	D59253	PASS	5	5.80	fail	3	5		Disease	Disease			NCBP Interacting Protein 1	RNA-binding protein that has two RNP consensus motifs
ITGB3	HG2320-HT3	HG2320-HT3	PASS	5	11.60	fail	3	5		Disease	Disease				
M33684_s_a	M33684_s_a	M33684	PASS	5	6.60	fail	3	5		Disease	Disease	PTPN1		non-receptor tyrosine phosphatase 1	
MYH10_r	U34301_r	U34301	PASS	5	15.40	fail	3	5		Disease	Disease				
X07438_s	X07438_s	X07438	PASS	5	9.00	fail	3	5		Disease	Disease				
CREB1	X68994_at	X68994	PASS	5	5.60	fail	3	5		Disease	Disease	CREB		Y protein	
MYL2	J02854_at	J02854	PASS	5	26.00	fail	2	5		Disease	Disease	MYL2		myosin light chain 2	
AC1	D82070_at	D82070	PASS	5	5.00	fail	2	5		Disease	Disease	aC1			
CGM7	D90276_at	D90276	PASS	5	14.60	fail	2	5		Disease	Disease	CGM7	19q13.2	carcinoembryonic antigen gene family member 7	carcinoembryonic antigen gene family member 7
HG4020-HT3	HG4020-HT3	HG4020-HT3	PASS	5	16.00	fail	2	5		Disease	Disease				
PCK1	L05144_at	L05144	PASS	5	5.60	fail	2	5		Disease	Disease	PCK1	20q13.31	phosphoenolpyruvate carboxykinase 1 (soluble)	phosphoenolpyruvate carboxykinase 1 (soluble)
DEFA5_ma1	M97925_ma	M97925	PASS	5	9.00	fail	2	5		Disease	Disease	DEFA5	8pter-p21	defensin 5	defensin, alpha 5, Paneth cell-specific
CCNG1IP	U61836_at	U61836	PASS	5	8.80	fail	2	5		Disease	Disease				
KRT3	X82634_at	X82634	PASS	5	6.40	fail	2	5		Disease	Disease	KRTA7	17q12-q21	keratin, hair, acidic, 7	keratin, hair, acidic, 7
NMOR2	J02888_at	J02888	PASS	7	12.71	PASS	8	7		1.99	1.99	NMOR2	6pter-q12	NAD(P)H menadiene oxidoreductase 2, dioxin-inducible	NAD(P)H menadiene oxidoreductase 2, dioxin-inducible
HG33-HT33	HG33-HT33	HG33-HT33	PASS	9	309.00	PASS	13	9		1.99	1.99				
RES422B	AB000460_a	AB000460	PASS	9	27.56	PASS	12	9		1.99	1.99	RES4-22	4p16.3	gene with multiple splice variants near HD locus on 4p16.3	gene with multiple splice variants near HD locus on 4p16.3
MIC2	M16279_at	M16279	PASS	9	72.22	PASS	13	9		1.99	1.99	MIC2	Xp22.32; Yp11.3	antigen identified by monoclonal antibodies 12E7, F21 and O13	antigen identified by monoclonal antibodies 12E7, F21 and O13
RB1	L22342_at	L22342	PASS	9	27.33	PASS	12	9		1.99	1.99	IF175		interferon-induced protein 75, 52kD	interferon-induced protein 75, 52kD
HLA-DNA	M31525_at	M31525	PASS	6	13.50	PASS	10	6		1.99	1.99	HLA-DNA		MHC HLA-DNA precursor	MHC HLA-DNA precursor
LRP1	X79882_at	X79882	PASS	7	27.29	PASS	12	7		1.98	1.98	LRP		lung resistance-related protein	lung resistance-related protein
RAGE_cds3	U89336_cds3	U89336	PASS	9	12.56	PASS	12	9		1.98	1.98	HBX2		homeobox PBX2 gene	intron-exon boundaries identified by a contig of ESTs with GenBank Accession Numbers W76064, R59617, W72507

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J03805_s_at	J03805_s_at	J03805	PASS	9	14.33	PASS	13	9	7.23	1.98	1.98	8p12-p11.2	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform
ATOX1	U70660_at	U70660	PASS	8	13.38	PASS	12	8	6.75	1.98	1.98	5q32-q33	ATX1 (antioxidant protein 1, yeast) homolog 1	ATX1 (antioxidant protein 1, yeast) homolog 1
K22	D14664_at	D14664	PASS	8	16.50	PASS	12	8	8.33	1.98	1.98	KIAA0022	KIAA0022 gene product	KIAA0022 gene product
SMS	Z49099_at	Z49099	PASS	9	20.44	PASS	12	9	10.33	1.98	1.98	Xp22.1	spermine synthase	spermine synthase
TCFEL1	D50663_at	D50663	PASS	8	22.75	PASS	12	8	11.50	1.98	1.98	TCFEL1	similar to murine Tctel1 gene product	similar to murine Tctel1 gene product
CSTF3	U15782_at	U15782	PASS	8	11.38	PASS	12	8	5.75	1.98	1.98	CSTF3	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD
PLI	M11119_at	M11119	PASS	7	15.00	PASS	12	7	7.58	1.98	1.98	GLUD1	pseudo-env cds /pseudo	pseudo-env cds /pseudo
M20867_s_at	M20867_s_at	M20867	PASS	8	14.13	PASS	13	8	7.15	1.97	1.97	GLUD1	glutamate dehydrogenase precursor	glutamate dehydrogenase precursor
G6PD	M24470_at	M24470	PASS	9	15.78	PASS	11	9	8.00	1.97	1.97	GMPR	glucose-6-phosphate dehydrogenase	glucose-6-phosphate dehydrogenase
K24_PTDS	D14694_at	D14694	PASS	9	41.11	PASS	13	9	20.85	1.97	1.97	KIAA0024	guanosine monophosphate reductase	guanosine monophosphate reductase
REQ	U94585_at	U94585	PASS	9	19.11	PASS	13	9	9.69	1.97	1.97	hsReq	KIAA0024 gene product	KIAA0024 gene product
L19493_s_at	L19493_s_at	L19493	PASS	7	9.86	PASS	11	7	5.00	1.97	1.97	FMRI	zinc finger; contains one C2H2 and two C4HC3	zinc finger; contains one C2H2 and two C4HC3
M12959_s_at	M12959_s_at	M12959	PASS	9	13.72	PASS	13	9	69.62	1.97	1.97	TCRA	T-cell receptor alpha-chain (VDIC)	T-cell receptor alpha-chain (VDIC)
TRSP	M86752_at	M86752	PASS	8	16.13	PASS	11	8	8.18	1.97	1.97	IEF SSP 3521	transformation-sensitive protein	transformation-sensitive protein
MYCBP	D89667_at	D89667	PASS	9	114.11	PASS	13	9	57.92	1.97	1.97	PFN5	prefoldin 5	prefoldin 5
MYL6	HG2815-HT2	HG2815-H	PASS	9	292.33	PASS	13	9	148.46	1.97	1.97	STIM1	stromal interaction molecule 1	stromal interaction molecule 1
GOK	U52426_at	U52426	PASS	7	14.00	PASS	9	7	7.11	1.97	1.97	ALDH9	aldehyde dehydrogenase 9 (gamma-aminobutyraldehyde dehydrogenase, E3 isozyme)	aldehyde dehydrogenase 9 (gamma-aminobutyraldehyde dehydrogenase, E3 isozyme)
ALDH7	U34252_at	U34252	PASS	8	13.63	PASS	13	8	6.92	1.97	1.97	ETFB	electron-transfer-flavoprotein, beta polypeptide	electron-transfer-flavoprotein, beta polypeptide
ETFB	X71129_at	X71129	PASS	9	12.00	PASS	10	9	6.10	1.97	1.97	dipA	hepatitis delta antigen interacting protein A	hepatitis delta antigen interacting protein A
DIPA	U63825_at	U63825	PASS	8	21.63	PASS	13	8	11.00	1.97	1.97	NAGA	N-acetylgalactosaminidase, alpha-	N-acetylgalactosaminidase, alpha-
NAGA	M62783_at	M62783	PASS	9	16.44	PASS	13	9	8.38	1.96	1.96	KIAA0317	KIAA0317 gene product	KIAA0317 gene product
K317	AB002315_at	AB002315	PASS	9	11.11	PASS	12	9	5.67	1.96	1.96	GLB1	galactosidase, beta 1	galactosidase, beta 1
GLB1	M34423_at	M34423	PASS	9	17.11	PASS	11	9	8.73	1.96	1.96	CD34	ubiquitin conjugating enzyme	ubiquitin conjugating enzyme
CD34	L22005_at	L22005	PASS	6	12.00	PASS	8	6	6.13	1.96	1.96	chondroitin sulfate	chondroitin sulfate	chondroitin sulfate
AGC1	U16306_at	U16306	PASS	9	104.11	PASS	13	9	53.15	1.96	1.96	splice-variant precursor peptide	splice-variant precursor peptide	splice-variant precursor peptide
SNRPN	J04615_at	J04615	PASS	9	51.22	PASS	13	9	26.15	1.96	1.96	15q12	small nuclear ribonucleoprotein N	small nuclear ribonucleoprotein N
ECHS1	D13900_at	D13900	PASS	9	27.00	PASS	10	9	13.80	1.96	1.96	10q26.2-q26.3	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial
CD14	X13334_at	X13334	PASS	9	180.11	PASS	13	9	92.08	1.96	1.96	5q22-q32	CD14 antigen	CD14 antigen
S164	L40392_at	L40392	PASS	8	14.00	PASS	12	8	7.17	1.95	1.95	ORF: putative	ORF: putative	ORF: putative

LRPAP1	M63959_at	M63959	PASS	8	28.25	PASS	13	8	14.46	1.95	1.95	LRPAP1	4p16.3	low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor-associated protein 1)	low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor-associated protein 1)
TXBP151	U33821_at	U33821	PASS	9	32.56	PASS	13	9	16.69	1.95	1.95	U33821		tax1-binding protein	tax1-binding protein
K177_ADRD79999_at	D79999	D79999	PASS	6	25.50	PASS	13	6	13.08	1.95	1.95	K1AA0177		ribose synthase, has putative hydrophobic domain in amino acid positions 638-662.	ribose synthase, has putative hydrophobic domain in amino acid positions 638-662.
MOZ	U47742_at	U47742	PASS	9	26.67	PASS	13	9	13.69	1.95	1.95	MOZ		monocytic leukaemia zinc finger protein	monocytic leukaemia zinc finger protein
HCG5	X81003_at	X81003	PASS	9	16.78	PASS	13	9	8.62	1.95	1.95	HCGV	6p21.3	hemochromatosis candidate gene V	hemochromatosis candidate gene V
J04130_s_at	J04130_s_at	J04130	PASS	9	27.56	PASS	13	9	14.15	1.95	1.95	SCYA4	17q21	small inducible cytokine A4 (homologous to mouse Mip-1b)	small inducible cytokine A4 (homologous to mouse Mip-1b)
H3F3B	M11353_at	M11353	PASS	9	245.78	PASS	13	9	126.31	1.95	1.95	H3FJ	6p22-p21.3	H3 histone family, member J	H3 histone family, member J
PSEN1	L76517_at	L76517	PASS	9	18.56	PASS	13	9	9.54	1.95	1.95	PSEN1	14q24.3	presenilin 1 (Alzheimer disease 3)	presenilin 1 (Alzheimer disease 3)
MGST2	U77604_at	U77604	PASS	8	19.00	PASS	13	8	9.77	1.94	1.94	MGST2	4q28-q31	microsomal glutathione S-transferase 2	microsomal glutathione S-transferase 2
MACS	D10522_at	D10522	PASS	8	13.75	PASS	13	8	7.08	1.94	1.94	MACS	6q21	myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K-L)	myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K-L)
PSMH3N3	D26600_at	D26600	PASS	9	46.78	PASS	13	9	24.08	1.94	1.94	PSMB4	1q21	proteasome (prosome, macropain) subunit, beta type, 4	proteasome (prosome, macropain) subunit, beta type, 4
MYL2	M21812_at	M21812	PASS	8	11.38	PASS	7	8	5.86	1.94	1.94	SHC		alternatively spliced isoform in p66shc	alternatively spliced isoform in p66shc
SKI	U73377_at	U73377	PASS	9	11.44	PASS	11	9	5.91	1.94	1.94	SHC		myosin light chain 2	myosin light chain 2
CLK2	L29218_at	L29218	PASS	7	13.71	PASS	11	7	7.09	1.93	1.93	CLK2	1q21	CDC-like kinase 2	CDC-like kinase 2
PPBP	M54995_at	M54995	PASS	9	251.56	PASS	13	9	130.31	1.93	1.93	PPBP	4q12-q13	pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2)	pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2)
SDHA	L21936_at	L21936	PASS	9	23.44	PASS	13	9	12.15	1.93	1.93	SDHA	5p15	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)
UBA52	S79522_at	S79522	PASS	9	286.56	PASS	13	9	148.69	1.93	1.93	RPS27A	2	ribosomal protein S27a	ribosomal protein S27a
SARS	X91257_at	X91257	PASS	9	38.22	PASS	13	9	19.85	1.93	1.93	serS		seryl-tRNA synthetase	seryl-tRNA synthetase
GPS2	U28963_at	U28963	PASS	8	13.63	PASS	13	8	7.08	1.93	1.93	GPS2		G protein pathway suppressor 2	G protein pathway suppressor 2
ELANH2	M91056_at	M91056	PASS	8	16.13	PASS	13	8	8.38	1.92	1.92	ELANH2	6p25	protease inhibitor 2 (anti-elastase), monocytic/neutrophil	protease inhibitor 2 (anti-elastase), monocytic/neutrophil
NT5	D38524_at	D38524	PASS	8	10.00	PASS	10	8	5.20	1.92	1.92	5'-nucleotidase		putative	putative
ATP5O	S77356_at	S77356	PASS	9	21.00	PASS	13	9	10.92	1.92	1.92	transcript ch21		oligomycin sensitivity conferral protein oscp homolog. This sequence comes from Fig. 3. Protein sequence is in conflict with the conceptual translation; insertions(7-9, missing Y)	oligomycin sensitivity conferral protein oscp homolog. This sequence comes from Fig. 3. Protein sequence is in conflict with the conceptual translation; insertions(7-9, missing Y)
K58	D31767_at	D31767	PASS	9	108.22	PASS	13	9	56.31	1.92	1.92	K1AA0058		K1AA0058 gene product	K1AA0058 gene product

# Table 2001

YY1	M77698 at	M77698	PASS	9	13.44	PASS	9	7.00	1.92	1.92	YY1	14q	YY1 transcription factor	YY1 transcription factor
POLR2	U37690 at	U37690	PASS	9	51.56	PASS	13	26.85	1.92	1.92	hsRPB10		RNA polymerase II subunit	
CR3p211GS	L13434 at	L13434	PASS	6	12.00	PASS	8	6.25	1.92	1.92				
MEA	HG1869-HT	HG1869-H	PASS	9	19.33	PASS	13	10.08	1.92	1.92				
PSMC3	M34079 at	M34079	PASS	6	13.17	PASS	8	6.88	1.92	1.92	PSMC3	11p12-p13	proteasome (prosome, macropain) 26S subunit, ATPase, 3	proteasome (prosome, macropain) 26S subunit, ATPase, 3
CTGB43A	L10378 at	L10378	PASS	9	18.22	PASS	13	9.54	1.91	1.91				The ha2022 gene product is novel.
K84	D42043 at	D42043	PASS	9	26.00	PASS	13	13.62	1.91	1.91	KIAA0084			
UB mal	U49869 mal	U49869	PASS	9	329.78	PASS	13	173.00	1.91	1.91	CYBA	16q24	ubiquitin	cytochrome b-245, alpha polypeptide
CYBA	M21186 at	M21186	PASS	9	221.67	PASS	13	116.38	1.90	1.90			phosphoglycerate mutase 1 (brain)	phosphoglycerate mutase 1 (brain)
PGAM1	J04173 at	J04173	PASS	9	72.56	PASS	13	38.15	1.90	1.90	PGAM1	10q25.3		
M6PR mal	X56253 mal	X56253	PASS	9	46.33	PASS	13	24.38	1.90	1.90				
ITGB5	J05633 at	J05633	PASS	7	9.29	PASS	9	4.89	1.90	1.90	ITGB5		integrin, beta 5	integrin, beta 5
U68105 s at	U68105 s at	U68105	PASS	9	97.56	PASS	13	51.38	1.90	1.90				
ADAR	U10439 at	U10439	PASS	9	34.56	PASS	13	18.23	1.90	1.90	ADAR	1q21.1-q21.2	adenosine deaminase, RNA-specific	adenosine deaminase, RNA-specific
TP53BP2	U58334 at	U58334	PASS	6	12.00	PASS	12	6.33	1.89	1.89	TP53BP2	1q42.1	Bbp/53BP2	tumor protein p53-binding protein, 2
K135_PIM1	D50925 at	D50925	PASS	6	12.00	PASS	9	6.33	1.89	1.89	KIAA0135			The KIAA0135 gene is related to p11n-1 oncogene.
EWSR1	X71428 at	X71428	PASS	9	72.00	PASS	13	38.00	1.89	1.89	FUS	16p11.2	FUS glycine rich protein	fusion, derived from (12;16)
PSMD7	U70735 at	U70735	PASS	9	15.44	PASS	13	8.15	1.89	1.89			34 kDa Mov34 homolog	malignant liposarcoma similar to Mov34
ZAP112	L40399 at	L40399	PASS	6	26.50	PASS	10	14.00	1.89	1.89				ORF: putative
ALOX5	J03600 at	J03600	PASS	9	29.33	PASS	12	15.50	1.89	1.89	ALOX5	10q11.2	arachidonate 5-lipoxygenase	arachidonate 5-lipoxygenase
MEN1	U93237 mal	U93237	PASS	6	11.67	PASS	12	6.17	1.89	1.89	MEN1	11q13	multiple endocrine neoplasia 1	multiple endocrine neoplasia 1
K262	D87451 at	D87451	PASS	9	54.89	PASS	13	29.08	1.89	1.89	KIAA0262			KIAA0262 gene product
X55448 cds	X55448 cds	X55448	PASS	9	27.44	PASS	13	14.54	1.89	1.89	G6PD		glucose-6-phosphate dehydrogenase	
E_23745	U79260 at	U79260	PASS	6	12.33	PASS	11	6.55	1.88	1.88				similar to human oligodendrocyte myelin glycoprotein encoded by GenBank Accession Number L05367
CBOG3955	D87119 at	D87119	PASS	8	19.75	PASS	12	10.50	1.88	1.88			GS3955	
BLVRA	U34877 at	U34877	PASS	8	14.88	PASS	12	7.92	1.88	1.88	BLVRA	7p14-cen	biliverdin reductase A	biliverdin reductase A
HEXB	M23294 at	M23294	PASS	6	20.67	PASS	12	11.00	1.88	1.88	HEXB	5q13	hexosaminidase B (beta polypeptide)	hexosaminidase B (beta polypeptide)
AC002045_x	AC002045_x	AC002045	PASS	9	25.00	PASS	13	13.31	1.88	1.88	A-589H1.1		Unknown protein product	
													CIT987SK-A-589H1_1 splice form 1	
NOL1	HG1116-HT	HG1116-H	PASS	7	12.86	PASS	13	6.85	1.88	1.88				
HG2090-HT2	HG2090-HT2	HG2090-H	PASS	9	16.89	PASS	11	9.00	1.88	1.88				
NDUFA4	U94586 at	U94586	PASS	9	32.44	PASS	13	17.31	1.87	1.87	NDUFA4		NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4 (9KD, MLRQ)
K59_DMT	D31883 at	D31883	PASS	9	45.56	PASS	13	24.31	1.87	1.87	LIMAB1	10q25	LIM actin binding protein 1 (limatin)	LIM actin binding protein 1 (limatin)
3P25MP	L09260 at	L09260	PASS	9	16.11	PASS	13	8.62	1.87	1.87				

# FOFET database

YWHAZ	M86400_at	M86400	PASS	9	116.22	PASS	13	9	62.15	1.87	1.87	YWHAZ	2p25.2-p25.1	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
Z74792_s_at	Z74792_s_at	Z74792	PASS	5	10.80	PASS	9	5	5.78	1.87	1.87			CCAAT transcription binding factor, gamma subunit	CCAAT transcription binding factor, gamma subunit
HBG2_mal	M91036_mal	M91036	PASS	9	60.56	PASS	12	9	32.42	1.87	1.87	HBG1	1p15.5	hemoglobin, gamma A	hemoglobin, gamma A
COX6B_cds	AC002115_c	AC002115	PASS	9	114.11	PASS	13	9	61.23	1.86	1.86	COX6B		F25451_2	hypothetical 36.5 kDa protein most similar to ssRNA binding proteins; BLASTX similarity to (Y07952) ssRNA-binding protein (Dictyostelium discoideum) (52%) within RNP domains; and to (Z70043) hypothetical 24.4 kD protein C22E12.02 in chromosome I (Schizosaccharomyces pombe)
PSMHSC10	D26598_at	D26598	PASS	9	45.56	PASS	13	9	24.46	1.86	1.86	PSMB3	2q35	proteasome (prosome, macropain) subunit, beta type, 3	proteasome (prosome, macropain) subunit, beta type, 3
M14328_s_at	M14328_s_at	M14328	PASS	9	173.22	PASS	13	9	93.15	1.86	1.86	ENO1	1p36.2-p36.3	enolase 1, (alpha)	enolase 1, (alpha)
CAPN2	M23254_at	M23254	PASS	9	63.33	PASS	13	9	34.08	1.86	1.86	CAPN2	1	calpain, large polypeptide L2	calpain, large polypeptide L2
HG110-HT1	HG110-HT1	HG110-HT1	PASS	9	26.44	PASS	13	9	14.23	1.86	1.86				
U45448_s_at	U45448_s_at	U45448	PASS	8	13.63	PASS	12	8	7.33	1.86	1.86	P2RX1	17p	purinergic receptor P2X, ligand-gated ion channel, 1	purinergic receptor P2X, ligand-gated ion channel, 1
K275_SPOC1	D87465_at	D87465	PASS	9	50.44	PASS	13	9	27.15	1.86	1.86	KIAA0275		KIAA0275 gene product	KIAA0275 gene product
NCL_mal	M60858_mal	M60858	PASS	9	73.00	PASS	13	9	39.31	1.86	1.86	NCL	2q12-qter	nucleolin	nucleolin
IRATHL60N	U09196_at	U09196	PASS	9	27.00	PASS	13	9	14.54	1.86	1.86				
CPBP	U44975_at	U44975	PASS	8	13.00	PASS	11	8	7.00	1.86	1.86	COPEB	10p15	core promoter element binding protein	core promoter element binding protein
ATP5G1	D13118_at	D13118	PASS	9	37.44	PASS	12	9	20.17	1.86	1.86	ATP5G3	2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3
EIF3	U36764_at	U36764	PASS	9	25.33	PASS	13	9	13.69	1.85	1.85	EIF3S2	1p34.1	eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD)	eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD)
XBP1	M31627_at	M31627	PASS	9	33.00	PASS	13	9	17.85	1.85	1.85	XBP1	22		X-box binding protein 1
HLA-A_f	HG3597-HT1	HG3597-H	PASS	9	182.11	PASS	13	9	98.62	1.85	1.85				
K77	D38521_at	D38521	PASS	9	11.67	PASS	12	9	6.33	1.84	1.84	KIAA0077			The ha0919 gene product is novel.
KPNB1	L38951_at	L38951	PASS	7	15.86	PASS	13	7	8.62	1.84	1.84	KPNB1		karyopherin (importin) beta 1	karyopherin (importin) beta 1
NDP52	U22897_at	U22897	PASS	9	14.22	PASS	11	9	7.73	1.84	1.84	ndp52		nuclear domain 10 protein as characterized by a monoclonal antibody recognizing the encoded protein	nuclear domain 10 protein as characterized by a monoclonal antibody recognizing the encoded protein
ARF1	M84332_at	M84332	PASS	9	115.56	PASS	13	9	62.85	1.84	1.84	ARF1	1q42	ADP-ribosylation factor 1	ADP-ribosylation factor 1
DAD1	D15057_at	D15057	PASS	9	20.22	PASS	13	9	11.00	1.84	1.84	DAD1	14q11-q12	defender against cell death 1	defender against cell death 1
PP1A_mal	X52851_mal	X52851	PASS	9	139.56	PASS	13	9	75.92	1.84	1.84			peptidylprolyl isomerase	
PPP2R56A	L42373_at	L42373	PASS	9	17.78	PASS	13	9	9.69	1.83	1.83	PPP2R5A	1q41	protein phosphatase 2A B56-alpha	protein phosphatase 2, regulatory subunit B (B56), alpha isoform
EIF4C	L18960_at	L18960	PASS	9	11.00	PASS	11	9	6.00	1.83	1.83	EIF4AY	Y chr.	eukaryotic translation initiation factor 1A, Y chromosome	eukaryotic translation initiation factor 1A, Y chromosome

# TOTAL "T54E00"

GCH1	U19523_at	U19523	PASS	7	10.86	PASS	13	7	5.92	1.83	1.83	GCH1	14q22.1-q22.2	GTP cyclohydrolase 1 (dopa-responsive dystonia)
CD37	X14046_at	X14046	PASS	9	74.67	PASS	13	9	40.77	1.83	1.83	CD37	19p13-q13.4	CD37 antigen
K240	D87077_at	D87077	PASS	6	9.33	PASS	10	6	5.10	1.83	1.83	KIAA0240		
M24485_s_a	M24485_s_a	M24485	PASS	9	80.33	PASS	13	9	43.92	1.83	1.83	GSTP1	11q13	glutathione S-transferase pi
HSPD1	M22382_at	M22382	PASS	9	31.22	PASS	13	9	17.08	1.83	1.83	HSPD1		heat shock 60kD protein 1 (chaperonin)
D26156_s_a	D26156_s_a	D26156	PASS	8	13.63	PASS	13	8	7.46	1.83	1.83	SMARCA4		SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4
HLA-C_f	HG658-HT6	HG658-HT	PASS	9	320.78	PASS	13	9	175.77	1.82	1.82			
HLA-E_f	HG2917-HT	HG2917-H	PASS	9	248.00	PASS	13	9	136.00	1.82	1.82			
K34_CLTCL	D21260_at	D21260	PASS	9	23.00	PASS	13	9	12.62	1.82	1.82	CLTCL2		clathrin, heavy polypeptide-like 2
PRKCD	D10495_at	D10495	PASS	9	30.22	PASS	12	9	16.58	1.82	1.82	35550		protein kinase C delta-type
M37238_s_a	M37238_s_a	M37238	PASS	9	11.33	PASS	9	9	6.22	1.82	1.82	PLCG2	16q24.1	phospholipase C, gamma 2 (phosphatidylinositol-specific)
REK1	AJ001421_at	AJ001421	PASS	9	33.89	PASS	13	9	18.62	1.82	1.82			Rer1 protein
PPR1A	HG1614-HT	HG1614-H	PASS	9	106.56	PASS	13	9	58.62	1.82	1.82			protein phosphatase 2A, regulatory subunit B (PR 53)
PPP2R4	U37352_at	U37352	PASS	7	12.57	PASS	13	7	6.92	1.82	1.82	PPP2R4	9q34	protein phosphatase 2A, regulatory subunit B (PR 53)
HUNC18B2	AB002559_a	AB002559	PASS	8	21.63	PASS	11	8	11.91	1.82	1.82			putative alternatively spliced form of gblU63533HSU63533
J03077_s_at	J03077_s_at	J03077	PASS	9	339.89	PASS	13	9	187.54	1.81	1.81	PSAP	10q21-q22	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)
ARRB2	HG2059-HT2	HG2059-H	PASS	9	24.67	PASS	13	9	13.62	1.81	1.81			
E_23652	U90911_at	U90911	PASS	9	13.00	PASS	11	9	7.18	1.81	1.81			
HG1595-HT4	HG1595-HT4	HG1595-H	PASS	8	26.00	PASS	13	8	14.38	1.81	1.81			
CSNK1D	U29171_at	U29171	PASS	9	18.22	PASS	12	9	10.08	1.81	1.81	CSNK1D	17q25	casein kinase I, delta
RPS3A	M84711_at	M84711	PASS	9	298.78	PASS	13	9	165.62	1.80	1.80	RPS3A	4q31.2-q31.3	ribosomal protein S3A
GLUL	X59834_at	X59834	PASS	9	23.00	PASS	12	9	12.75	1.80	1.80	GLUL	1q31	glutamate-ammonia ligase (glutamine synthase)
IL4R	X52425_at	X52425	PASS	9	26.22	PASS	11	9	14.55	1.80	1.80	IL4R	16p11.2-p12.1	interleukin 4 receptor
CSTB_maf	U46692_maf	U46692	PASS	9	47.22	PASS	13	9	26.23	1.80	1.80	CSTB	21q22.3	cystatin B (stefin B)
M22348_s_a	M22348_s_a	M22348	PASS	8	11.38	PASS	9	8	6.33	1.80	1.80	UQB		ubiquitin-binding protein precursor
RPS17	M18000_at	M18000	PASS	9	464.56	PASS	13	9	238.69	1.80	1.80	RPS17	11pter-p13 or 15q	ribosomal protein S17
RPLP0	M17885_at	M17885	PASS	9	436.11	PASS	13	9	243.00	1.79	1.79	RPLP0	12	ribosomal protein, large, P0
YRS28	D14530_at	D14530	PASS	9	367.89	PASS	13	9	205.31	1.79	1.79	RPS23	5q	ribosomal protein S23
CBFB	L20298_at	L20298	PASS	9	21.78	PASS	13	9	12.15	1.79	1.79	CBFB	16q22.1	core-binding factor, beta subunit
CANX	L10284_at	L10284	PASS	9	41.89	PASS	13	9	23.38	1.79	1.79	CANX	5q35	calnexin
HLARK	U89505_at	U89505	PASS	8	17.75	PASS	13	8	9.92	1.79	1.79	RBM4	11q13	RNA binding motif protein 4
ZFP	U69645_at	U69645	PASS	8	10.13	PASS	12	8	5.67	1.79	1.79			C2H2 type zinc finger
SUI1	L26247_at	L26247	PASS	9	177.22	PASS	13	9	99.38	1.78	1.78	sui1ol		isolates of yeast sui1 and rice gos2; putative
VDAC1	L06132_at	L06132	PASS	8	15.50	PASS	13	8	8.69	1.78	1.78	VDAC1	5q31	voltage-dependent anion channel 1
L12711_s_at	L12711_s_at	L12711	PASS	9	67.89	PASS	13	9	38.08	1.78	1.78	TKT	3p14.3	transketolase (Wernicke-Korsakoff syndrome)

# Table 1

EIF4A1	D13748_at	D13748	PASS	9	107.22	PASS	13	9	60.15	1.78	1.78	1.78	EIF4A1	17p13	eukaryotic translation initiation factor 4A, isoform 1	eukaryotic translation initiation factor 4A, isoform 1
STAT13	AFFX-HUM	AFFX-HUN	PASS	9	23.44	PASS	13	9	13.15	1.78	1.78	1.78	POLR2G	11q13.1	polymerase (RNA) II (DNA directed) polypeptide G	polymerase (RNA) II (DNA directed) polypeptide G
POLR2G_ma	U52427_ma	U52427	PASS	9	29.56	PASS	12	9	16.58	1.78	1.78	1.78	AHCY	20cen-q13.1	S-adenosylhomocysteine hydrolase	S-adenosylhomocysteine hydrolase
M61832_s_a	M61832_s_a	M61832	PASS	7	10.29	PASS	9	7	5.78	1.78	1.78	1.78	ADPRT	1q41-q42	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)
HSPA9	L11066_at	L11066	PASS	9	28.33	PASS	13	9	15.92	1.78	1.78	1.78	KIAA0178		match D80000; similar to mitosis-specific chromosome segregation protein SMC1 of S. cerevisiae	match D80000; similar to mitosis-specific chromosome segregation protein SMC1 of S. cerevisiae
SMC1_xp2	Z97054_xp2	Z97054	PASS	6	10.00	PASS	8	6	5.63	1.78	1.78	1.78	RPL34	4 or 17	ribosomal protein L34	ribosomal protein L34
RPL34	L38941_at	L38941	PASS	9	432.56	PASS	13	9	243.62	1.78	1.78	1.78	AMPHL	2q14	amphiphysin-like	amphiphysin-like
HLA-E_f	HG2915-HT	HG2915-H	PASS	9	245.00	PASS	13	9	138.15	1.77	1.77	1.77	MGAT1	5	mannosyl (alpha-1,3-) glycoprotein beta-1,2-N-acetylglucosaminyltransferase	mannosyl (alpha-1,3-) glycoprotein beta-1,2-N-acetylglucosaminyltransferase
AMPHL	U68485_at	U68485	PASS	5	29.40	PASS	12	5	16.58	1.77	1.77	1.77	PDHAI	Xp22.1	pyruvate dehydrogenase (lipoamide) alpha 1	pyruvate dehydrogenase (lipoamide) alpha 1
MGAT1	M55621_at	M55621	PASS	8	18.13	PASS	13	8	10.23	1.77	1.77	1.77	COX4	16q22-qter	cytochrome c oxidase subunit IV	cytochrome c oxidase subunit IV
PDHAI	D90084_at	D90084	PASS	8	10.63	PASS	9	8	6.00	1.77	1.77	1.77	COPINE1		copine 1	copine 1
COX4	U90915_at	U90915	PASS	9	104.44	PASS	13	9	59.00	1.77	1.77	1.77	G10		maternal G10 transcript	maternal G10 transcript
COPINE1	U83246_at	U83246	PASS	9	49.11	PASS	13	9	27.77	1.77	1.77	1.77	KIAA0096		KIAA0096 gene product is related to a protein kinase	KIAA0096 gene product is related to a protein kinase
EDG2	U11861_at	U11861	PASS	9	38.89	PASS	13	9	22.00	1.77	1.77	1.77	UFD2	11	homolog of yeast (S. cerevisiae) ufd2	homolog of yeast (S. cerevisiae) ufd2
K96_PK	D43636_at	D43636	PASS	9	15.89	PASS	13	9	9.00	1.77	1.77	1.77	RPS6	9p21	ribosomal protein S6	ribosomal protein S6
K126_UB	D50916_at	D50916	PASS	8	13.00	PASS	11	8	7.36	1.77	1.77	1.77	SORL1	11q23.2-q24.4	sortilin-related receptor, L(DLR class) A repeats-containing	sortilin-related receptor, L(DLR class) A repeats-containing
E23682	U79288_at	U79288	PASS	8	19.13	PASS	12	8	10.83	1.77	1.77	1.77	TPRDI		FYN oncogene related to SRC, FGR, YES	FYN oncogene related to SRC, FGR, YES
RPS6_ma1	M77232_ma	M77232	PASS	9	274.44	PASS	13	9	155.46	1.77	1.77	1.77	TBCC		tubulin-specific chaperone c	tubulin-specific chaperone c
GP250	U60975_at	U60975	PASS	9	63.00	PASS	13	9	35.69	1.77	1.77	1.77	IL10RA	11q23	interleukin 10 receptor, alpha	interleukin 10 receptor, alpha
TTC3	D84294_at	D84294	PASS	9	16.56	PASS	13	9	9.38	1.76	1.76	1.76	E2F3	6p22	E2F transcription factor 3	E2F transcription factor 3
FYN	M14676_at	M14676	PASS	9	31.89	PASS	13	9	18.08	1.76	1.76	1.76	FBP1		fructose-1,6-bisphosphatase	fructose-1,6-bisphosphatase
TUBFOLD	U61234_at	U61234	PASS	8	11.38	PASS	11	8	6.45	1.76	1.76	1.76	DHPS		deoxyhypusine synthase	deoxyhypusine synthase
IL10R	U00672_at	U00672	PASS	9	30.22	PASS	13	9	17.15	1.76	1.76	1.76	IGHM	14q32.33	immunoglobulin mu	immunoglobulin mu
HG1400-HT	HG1400-HT	HG1400-H	PASS	9	11.78	PASS	13	9	6.69	1.76	1.76	1.76	KIAA0200		KIAA0200 gene product	KIAA0200 gene product
K75_E2F3	D38550_at	D38550	PASS	9	10.56	PASS	10	9	6.00	1.76	1.76	1.76	EEF1D		eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
FBP1	U21931_at	U21931	PASS	9	23.67	PASS	13	9	13.46	1.76	1.76	1.76				
DHPS	U79262_at	U79262	PASS	8	14.88	PASS	13	8	8.46	1.76	1.76	1.76				
IGHM	X38529_at	X38529	PASS	9	112.11	PASS	13	9	63.85	1.76	1.76	1.76				
K200_MAM	D83785_at	D83785	PASS	8	12.88	PASS	12	8	7.33	1.76	1.76	1.76				
EEF1D	Z21507_at	Z21507	PASS	9	104.11	PASS	13	9	59.31	1.76	1.76	1.76				
HG2259-HT2	HG2259-HT2	HG2259-H	PASS	9	67.44	PASS	13	9	38.54	1.75	1.75	1.75	FUCA1	1p34	fucoylidase, alpha-L-1, tissue	fucoylidase, alpha-L-1, tissue
FUCA1	M29877_at	M29877	PASS	8	14.00	PASS	13	8	8.00	1.75	1.75	1.75				



SELL	M25280_at	M25280	PASS	9	130.11	PASS	13	9	74.38	1.75	1.75	LNHR	Iq12-q22	S100 calcium-binding protein A9 (calgranulin B)	lymph node homing receptor precursor
M2631_s_at	M2631_s_at	M2631	PASS	9	301.44	PASS	13	9	172.38	1.75	1.75	S100A9	Iq12-q22	S100 calcium-binding protein A9 (calgranulin B)	
ANX2	D00017_at	D00017	PASS	9	88.33	PASS	13	9	50.62	1.75	1.75	ANX2	15q21-q22	annexin II (lipocortin II); calpactin 1, heavy polypeptide	annexin II (lipocortin II); calpactin 1, heavy polypeptide
K257_COSC	D87446_at	D87446	PASS	9	9.89	PASS	12	9	5.67	1.75	1.75	KIAA0257		Similar to a C elegans protein encoded in cosmid C27F2 (U40419)	Similar to a C elegans protein encoded in cosmid C27F2 (U40419)
K239_K215	D87076_at	D87076	PASS	7	19.00	PASS	10	7	10.90	1.74	1.74	KIAA0239		similar to human bromodomain protein BR140(JC2069)	similar to human bromodomain protein BR140(JC2069)
S78771_s_at	S78771_s_at	S78771	PASS	6	12.00	PASS	10	6	6.90	1.74	1.74			coronin homologue	
X89109_s_at	X89109_s_at	X89109	PASS	9	107.22	PASS	13	9	61.69	1.74	1.74				
S82447_s_at	S82447_s_at	S82447	PASS	8	10.25	PASS	10	8	5.90	1.74	1.74	GCN5L1	12q13-q14	GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 1	GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 1
FCN1	D83920_at	D83920	PASS	9	244.89	PASS	13	9	141.00	1.74	1.74	FCN1	9q34	ficollin (collagen/fibrinogen domain-containing) 1	ficollin (collagen/fibrinogen domain-containing) 1
HILA-DMB	U15085_at	U15085	PASS	9	54.22	PASS	13	9	31.23	1.74	1.74	HILA-DMB	6p21.3	major histocompatibility complex, class II, DM beta	major histocompatibility complex, class II, DM beta
CCND2	D13639_at	D13639	PASS	9	39.11	PASS	13	9	22.54	1.74	1.74	CCND2	12p13	cyclin D2	cyclin D2
CSNK1G2	U89896_at	U89896	PASS	6	9.83	PASS	9	6	5.67	1.74	1.74			casein kinase I gamma 2	
TAF2H	U13991_at	U13991	PASS	9	33.44	PASS	13	9	19.31	1.73	1.73	taf130		TATA-binding protein associated factor 30 kDa subunit	
M55409_s_at	M55409_s_at	M55409	PASS	9	258.78	PASS	13	9	149.46	1.73	1.73	EEF1G		eukaryotic translation elongation factor 1 gamma	eukaryotic translation elongation factor 1 gamma
W52B2_f	HG688-HT68	HG688-HT	PASS	8	61.25	PASS	13	8	35.38	1.73	1.73				
TRNASTL	U07424_at	U07424	PASS	7	14.00	PASS	11	7	8.09	1.73	1.73	FARSL		phenylalanine-tRNA synthetase like	phenylalanine-tRNA synthetase like
EIF2B	M29536_at	M29536	PASS	9	24.89	PASS	13	9	14.38	1.73	1.73	EIF2S2		eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD)	eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD)
E_23722	U90909_at	U90909	PASS	8	9.75	PASS	11	8	5.64	1.73	1.73				
LGALS3	M57710_at	M57710	PASS	9	66.89	PASS	13	9	38.69	1.73	1.73	LGALS3	1p13	lectin, galactoside-binding, soluble, 3 (galectin 3)	lectin, galactoside-binding, soluble, 3 (galectin 3)
PKUA	AB004884_a	AB004884	PASS	7	12.29	PASS	8	7	7.13	1.72	1.72			PKU-alpha	
J05016_mal	J05016_mal	J05016	PASS	8	9.88	PASS	11	8	5.73	1.72	1.72	ERP70	7; 10	protein disulfide isomerase related protein (calcium-binding protein, intestinal-related)	protein disulfide isomerase related protein (calcium-binding protein, intestinal-related)
Y09392_s_at	Y09392_s_at	Y09392	PASS	9	11.67	PASS	13	9	6.77	1.72	1.72	wsl1		WLS-S2 protein	truncated form of T-lymphocyte-specific protein tyrosine kinase p56lck; this aberrant message encoding primarily the SH2 and SH3 domains of p56lck was observed by northern hybridization and PCR amplification in poly-A selected RNA from two human leukemic T-cell lines.
U23852_s_at	U23852_s_at	U23852	PASS	9	66.89	PASS	13	9	38.85	1.72	1.72	lck		p56lck	

P4HB	J02783_at	J02783	PASS	5	30.20	PASS	11	5	17.55	1.72	1.72	P4HB	17q25	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55)	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55)	
DYRK	D86550_at	D86550	PASS	9	18.67	PASS	13	9	10.85	1.72	1.72	hMNB		serine/threonine protein kinase	human homolog of Drosophila mmb (numbrin) gene	
PSMCI	L02426_at	L02426	PASS	9	25.67	PASS	13	9	14.92	1.72	1.72	PSMCI	19p13.3	proteasome (prosome, macropain) 26S subunit, ATPase, 1	proteasome (prosome, macropain) 26S subunit, ATPase, 1	
CDID	L38820_at	L38820	PASS	8	12.50	PASS	11	8	7.27	1.72	1.72	CDID		CDID antigen	CDID antigen	
RPL9	U09953_at	U09953	PASS	9	318.56	PASS	13	9	185.46	1.72	1.72	RPL9	4p13	ribosomal protein L9	ribosomal protein L9	
U59877_s_at	U59877_s_at	U59877	PASS	6	15.67	PASS	8	6	9.13	1.72	1.72	RAB31		low-Mr GTP-binding protein of the Rab subfamily	low-Mr GTP-binding protein of the Rab subfamily	
GALT	M60091_at	M60091	PASS	9	11.44	PASS	9	9	6.67	1.72	1.72	GALT		galactose-1-phosphate uridylyl transferase	galactose-1-phosphate uridylyl transferase	
MARS	X94754_at	X94754	PASS	9	13.33	PASS	13	9	7.77	1.72	1.72	MARS	12	yeast methionyl-tRNA synthetase homolog	methionine-tRNA synthetase	
SI53	L40391_at	L40391	PASS	9	26.44	PASS	12	9	15.42	1.72	1.72					
CCNI	D50310_at	D50310	PASS	9	99.33	PASS	13	9	57.92	1.71	1.71			cyclin 1		
K99_PUML	D43951_at	D43951	PASS	9	12.00	PASS	11	9	7.00	1.71	1.71	KIAA0099		KIAA0099 gene product		
SRI	M81637_at	M81637	PASS	8	9.00	PASS	8	8	5.25	1.71	1.71	grancalcin		grancalcin	putative	
NDUF58	U65579_at	U65579	PASS	6	9.00	PASS	8	6	5.25	1.71	1.71	NDUF58	11q13	NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH-coenzyme Q reductase)	NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH-coenzyme Q reductase)	
E_23693	U79254_at	U79254	PASS	9	20.56	PASS	13	9	12.00	1.71	1.71					
K272_HYPC	D87462_at	D87462	PASS	6	11.50	PASS	7	6	6.71	1.71	1.71	BAP1	3p21.31-p21.2	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	
A4	L09604_at	L09604	PASS	9	80.22	PASS	13	9	46.85	1.71	1.71	PLP2	Xp11.23	proteolipid protein 2 (colonic epithelium-enriched)	proteolipid protein 2 (colonic epithelium-enriched)	
SLC6A8_ma	U36341_ma	U36341	PASS	9	13.11	PASS	9	9	7.67	1.71	1.71	SLC6A8		creatine transporter	creatine transporter	
TFAP3D	U91930_at	U91930	PASS	9	20.11	PASS	13	9	11.77	1.71	1.71	ADTD	19p13.3	adaptin, delta	adaptin, delta	
SEPW1	U67171_at	U67171	PASS	9	25.89	PASS	13	9	15.15	1.71	1.71	SEPW1		selenoprotein W, 1	selenoprotein W, 1	
P542	L38696_at	L38696	PASS	6	17.33	PASS	13	6	10.15	1.71	1.71			autoantigen p542	huRab1; hnRNP C3; N-terminus similar to huRNP C	
ERCC5	X69978_at	X69978	PASS	8	12.88	PASS	9	8	7.56	1.70	1.70	ERCC5	13q22-q34	XPG complementing protein	excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome))	
ARF4	M36341_at	M36341	PASS	9	17.56	PASS	13	9	10.31	1.70	1.70	ARF4		ADP-ribosylation factor 4	ADP-ribosylation factor 4	
POLRMP	U75370_at	U75370	PASS	7	10.43	PASS	8	7	6.13	1.70	1.70	POLRMT	19p13.3	mitochondrial RNA polymerase (DNA directed)	polymyrase (RNA) mitochondrial (DNA directed)	
LUMAN	AF009368_at	AF009368	PASS	7	17.29	PASS	11	7	10.18	1.70	1.70			Luman		basic leucine zipper (BLZP) protein; binds to herpes simplex virus VP16 associated host cellular factor (HCF); member of CREB/ATF protein family; mouse LZIP homolog

# Table 3

SAP61	U08815_at	U08815	PASS	8	10.75	PASS	9	8	6.33	1.70	1.70	SAP 61	SAP 61	similar to yeast PRP9, Swiss-Prot Accession Number P19736
ITK	U10717_at	U10717	PASS	9	15.67	PASS	13	9	9.23	1.70	1.70		tyrosine kinase	2024-2555 unique domain; 2556-2708 SH3 domain; 2750-3044 SH2 domain (binds phosphotyrosine-containing proteins); 3095-3884 kinase domain (phosphorylation of tyrosine residues); putative
AFEX-HUM4	AFEX-HUM4	AFEX-HUM4	PASS	7	14.14	PASS	9	7	8.33	1.70	1.70			
EIF23	U94855_at	U94855	PASS	9	60.00	PASS	13	9	35.38	1.70	1.70	EIF3S5		eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD)
U50079_s_at	U50079_s_at	U50079	PASS	7	22.43	PASS	13	7	13.23	1.70	1.70		histone deacetylase HD1	similar to S. cerevisiae RPD3, a global transcriptional regulator; trapoxin receptor
ISG20	U88964_at	U88964	PASS	9	49.00	PASS	13	9	28.92	1.69	1.69	ISG20	15q26	interferon stimulated gene (20kD)
CD81	M33680_at	M33680	PASS	9	76.22	PASS	13	9	45.00	1.69	1.69	CD81	11p15	CD81 antigen (target of antiproliferative antibody 1)
U19713_s_at	U19713_s_at	U19713	PASS	9	45.33	PASS	13	9	26.77	1.69	1.69	IRT-1		interferon gamma responsive transcript
APRT_ma1	Y00486_ma1	Y00486	PASS	9	43.22	PASS	13	9	25.54	1.69	1.69	APRT	16q24	adenine phosphoribosyltransferase
NF45	U10323_at	U10323	PASS	9	24.33	PASS	13	9	14.38	1.69	1.69	ILF2		interleukin enhancer binding factor 2, 45kD
IP30	U03909_at	U03909	PASS	9	159.78	PASS	13	9	94.54	1.69	1.69			gamma-interferon-inducible protein precursor
ORF	M68864_at	M68864	PASS	9	36.78	PASS	13	9	21.77	1.69	1.69			ORF
RPL27A	U14968_at	U14968	PASS	9	369.33	PASS	13	9	218.85	1.69	1.69	RPL27A	11	ribosomal protein L27a
RENT1	D86988_at	D86988	PASS	9	27.11	PASS	13	9	16.08	1.69	1.69	RENT1	19	regulator of nonsense transcripts 1
MOV34L	D50063_at	D50063	PASS	9	19.11	PASS	12	9	11.33	1.69	1.69	PSMD7	16q23-q24	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog)
FHL1	U60115_at	U60115	PASS	9	10.89	PASS	13	9	6.46	1.69	1.69	FHL1	Xq27.2	cytochrome c oxidase subunit Vb
COX5B	M19961_at	M19961	PASS	8	35.88	PASS	13	8	21.31	1.68	1.68	COX5B	2cen-q13	cytochrome c oxidase subunit Vb
EIF4G2	U73824_at	U73824	PASS	9	48.56	PASS	13	9	28.85	1.68	1.68	EIF4G2	1p15	eukaryotic translation initiation factor 4 gamma, 2
K70_KARS	D31890_at	D31890	PASS	9	31.44	PASS	13	9	18.69	1.68	1.68	KIAA0070		similar to lysyl tRNA synthetase.
CD37L	U43077_at	U43077	PASS	9	24.44	PASS	13	9	14.54	1.68	1.68			similar to S. cerevisiae Cdc37p
SSBP	M94556_at	M94556	PASS	9	23.78	PASS	13	9	14.15	1.68	1.68	SSBP	7q34	single-stranded DNA-binding protein
RG33	U27655_at	U27655	PASS	8	8.25	PASS	12	8	4.92	1.68	1.68	RG33		ubiquitin specific protease 10
K190_UBP3	D80012_at	D80012	PASS	8	14.25	PASS	12	8	8.50	1.68	1.68	USP10		flightless 1 (Drosophila) homolog
FLI1_ma1	U80184_ma1	U80184	PASS	7	18.43	PASS	13	7	11.00	1.68	1.68	FLI1	17p11.2	flightless 1 (Drosophila) homolog
AIM1	U83115_at	U83115	PASS	9	20.44	PASS	13	9	12.23	1.67	1.67	AIM1	6q21	absent in melanoma 1
TATSF1	U76992_at	U76992	PASS	7	10.29	PASS	13	7	6.15	1.67	1.67	Tat-SF1		similar to EWS and FUS/TLS77

K235_K99	D87078_at	D87078	PASS	5	23.40	PASS	13	5	14.00	1.67	1.67	KIAA0235			similar to D.melanogaster pumilio protein (S22026); similar to human KIAA0099 protein(D43951)
HSPB1	U12404_at	U12404	PASS	9	340.44	PASS	13	9	203.69	1.67	1.67		Csa-19		
K205_COSC	D86960_at	D86960	PASS	9	9.89	PASS	12	9	5.92	1.67	1.67	KIAA0205			KIAA0205 gene product
CTBP1	U37408_at	U37408	PASS	9	19.67	PASS	13	9	11.77	1.67	1.67	CTBP1	4p16		C-terminal binding protein 1
EBVSRA	HG662-HT66	HG662-HT	PASS	9	150.89	PASS	13	9	90.38	1.67	1.67				
ARHGD1B	L20688_at	L20688	PASS	9	315.00	PASS	13	9	188.69	1.67	1.67	ARHGD1B	12p12.3		Rho GDP dissociation inhibitor (GDI) beta
LTA4H	J03459_at	J03459	PASS	9	78.78	PASS	13	9	47.23	1.67	1.67	LTA4H	12q22		leukotriene A4 hydrolase
ELP1	M88458_at	M88458	PASS	9	12.44	PASS	13	9	7.46	1.67	1.67				leukotriene A4 hydrolase
NP220	D83032_at	D83032	PASS	9	10.00	PASS	13	9	6.00	1.67	1.67				unsure initial methionine-putative
TAP	U80073_at	U80073	PASS	9	14.44	PASS	12	9	8.67	1.67	1.67	TAP			tip associating protein
EV12B	M60830_at	M60830	PASS	8	20.25	PASS	13	8	12.15	1.67	1.67				open reading frame
K249_K188	D87436_at	D87436	PASS	8	8.88	PASS	12	8	5.33	1.66	1.66	KIAA0249			KIAA0249 gene product
CIT987SK	U95740_ma	U95740	PASS	9	14.00	PASS	12	9	8.42	1.66	1.66	A-362G6.1			Unknown gene product
NASP	M97856_at	M97856	PASS	8	12.88	PASS	8	8	7.75	1.66	1.66	NASP			nuclear autoantigenic sperm protein (histone-binding)
K94_MEAP	D42084_at	D42084	PASS	8	11.63	PASS	13	8	7.00	1.66	1.66	KIAA0094			KIAA0094 gene product is related to Scerevisiae methionine aminopeptidase.
L10333_s_at	L10333_s_at	L10333	PASS	5	9.80	PASS	11	5	5.91	1.66	1.66	NSP			neuroendocrine-specific protein A
H2A1L	U90551_at	U90551	PASS	9	42.22	PASS	13	9	25.46	1.66	1.66	H2A1L			histone 2A-like protein
K49_LA13B	D30756_at	D30756	PASS	9	10.44	PASS	13	9	6.31	1.66	1.66	KIAA0049			KIAA0049 gene product
DNAPK	U85611_at	U85611	PASS	9	35.89	PASS	13	9	21.69	1.65	1.65	KIP			DNA-PK interaction protein
D13720_s_at	D13720_s_at	D13720	PASS	8	14.25	PASS	13	8	8.62	1.65	1.65				ITK
K241_COST	D63877_at	D63877	PASS	6	8.50	PASS	7	6	5.14	1.65	1.65	KIAA0157			originally named lyk KIAA0157 gene product is novel.
RCH1	U28386_at	U28386	PASS	7	8.86	PASS	11	7	5.36	1.65	1.65	KPNA2	17q23.1-q23.3		karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
K37_ADCY	D25538_at	D25538	PASS	9	17.78	PASS	13	9	10.77	1.65	1.65	ADCY7	16q12-q13		adenylate cyclase 7
RST	M24194_at	M24194	PASS	9	326.89	PASS	13	9	198.15	1.65	1.65	H12-3			homologue; putative nuclear phosphoprotein (similarity to Saccharomyces cerevisiae PWP1 protein)
IEFSSP9502	L07758_at	L07758	PASS	9	9.44	PASS	11	9	5.73	1.65	1.65				IEF SSP 9502
K53_CDC42	D29642_at	D29642	PASS	9	27.89	PASS	12	9	16.92	1.65	1.65	KIAA0053			KIAA0053 gene product
ABR	U01147_at	U01147	PASS	9	9.89	PASS	12	9	6.00	1.65	1.65	ABR	17p13.3		active BCR-related gene
SET	M93651_at	M93651	PASS	9	24.33	PASS	13	9	14.77	1.65	1.65	SET	9q34		SET translocation (myeloid leukemia-associated)
K38	D26068_at	D26068	PASS	9	54.22	PASS	13	9	32.92	1.65	1.65	WSCR1	7q11.23		Williams-Beuren syndrome chromosome region 1
PTPCAAX1	U48296_at	U48296	PASS	7	8.43	PASS	8	7	5.13	1.64	1.64	PTP4A1	6q12		Protein tyrosine phosphatase IVA, member 1
U01691_s_at	U01691_s_at	U01691	PASS	9	17.44	PASS	13	9	10.62	1.64	1.64	ANX5	4q28-q32		annexin V (endonexin II)
M16591_s_at	M16591_s_at	M16591	PASS	9	29.44	PASS	13	9	17.92	1.64	1.64	HCK	20q11-q12		hemopoietic cell kinase
K102_SPC25	D14658_at	D14658	PASS	9	22.11	PASS	13	9	13.46	1.64	1.64	KIAA0102			KIAA0102 gene product
E 23815	U90916_at	U90916	PASS	8	11.88	PASS	13	8	7.23	1.64	1.64				

NFE2L2	S74017_at	S74017	PASS	5	11.00	PASS	10	5	6.70	1.64	1.64	Nr2	Nr2	NF-E2-like basic leucine zipper transcriptional activator; This sequence comes from Fig. 1
MTH1	D16381_at	D16381	PASS	8	17.00	PASS	11	8	10.36	1.64	1.64	MTH1	7p22	mutT (E. coli) human homolog (8-oxo-7,8-dihydroguanosine triphosphatase)
FKHR	U36922_at	U36922	PASS	9	17.78	PASS	13	9	10.85	1.64	1.64			gene predicted from cDNA with a complete coding sequence
K105	D14661_at	D14661	PASS	7	8.57	PASS	13	7	5.23	1.64	1.64	KIAA0105	6	calpastatin
CAST	D16217_at	D16217	PASS	9	20.67	PASS	13	9	12.62	1.64	1.64	CAST	5q14-q22	calpastatin
K209	DOCK86964_at	D86964	PASS	9	20.78	PASS	13	9	12.69	1.64	1.64	DOCK2		dedicator of cyto-kinesis 2
X91911_s_at	X91911_s_at	X91911	PASS	8	21.13	PASS	13	8	12.92	1.63	1.63	rnp-1		
DAPM	AFEX-DapX	AFEX-Dap	PASS	9	505.56	PASS	13	9	309.31	1.63	1.63			
TCF7	X59871_at	X59871	PASS	9	45.22	PASS	13	9	27.69	1.63	1.63	TCF7	5q31	transcription factor 7 (T-cell specific, HMG-box)
RF513	HG821-HT8	HG821-HT	PASS	9	277.00	PASS	13	9	169.77	1.63	1.63			
X77588_s_at	X77588_s_at	X77588	PASS	8	10.88	PASS	12	8	6.67	1.63	1.63	ARD1	Xq28	N-acetyltransferase, homolog of S. cerevisiae ARD1
V00599_s_at	V00599_s_at	V00599	PASS	9	49.78	PASS	13	9	30.54	1.63	1.63			beta-tubulin
TP53	M22898_at	M22898	PASS	7	8.00	PASS	11	7	4.91	1.63	1.63	TP53	17p13.1	tumor protein p53 (Li-Fraumeni syndrome)
U31903_s_at	U31903_s_at	U31903	PASS	7	16.14	PASS	11	7	9.91	1.63	1.63	CREBL1	6p21.3	cAMP responsive element binding protein-like 1
SLC1A7	U33347_at	U33347	PASS	7	13.57	PASS	12	7	8.33	1.63	1.63			neural amino acid transporter
D13413_ma	D13413_ma	D13413	PASS	9	438.11	PASS	13	9	269.08	1.63	1.63	HNRPU		heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)
TGFB1	M77349_at	M77349	PASS	9	42.67	PASS	13	9	26.23	1.63	1.63	TGFB1	5q31	transforming growth factor, beta-induced, 68kD
K122	D50912_at	D50912	PASS	6	8.33	PASS	8	6	5.13	1.63	1.63	KIAA0122		The KIAA0122 gene product is novel.
AES	U04241_at	U04241	PASS	9	65.33	PASS	13	9	40.23	1.62	1.62	AES	19p13.3	amino-terminal enhancer of split
MAD3	M69043_at	M69043	PASS	9	41.33	PASS	13	9	25.46	1.62	1.62	NFKBIA	14q13	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha
NME2	HG1153-HT	HG1153-HT	PASS	9	42.00	PASS	13	9	25.92	1.62	1.62			
K26	D14812_at	D14812	PASS	9	36.44	PASS	12	9	22.50	1.62	1.62	KIAA0026		KIAA0026 gene product
HG4312-HT	HG4312-HT	HG4312-HT	PASS	9	48.33	PASS	13	9	29.85	1.62	1.62			
TCRG	M30894_at	M30894	PASS	9	19.56	PASS	13	9	12.08	1.62	1.62	CD3G		Ti antigen CD3-associated protein precursor
U05572_s_at	U05572_s_at	U05572	PASS	9	27.89	PASS	13	9	17.23	1.62	1.62	MANB	19cen-q13.1	alpha-mannosidase
M98399_s_at	M98399_s_at	M98399	PASS	8	15.38	PASS	12	8	9.50	1.62	1.62	CD36	7q1.2	CD36 antigen (collagen type I receptor, thrombospondin receptor)
BLVRB	D26308_at	D26308	PASS	9	36.00	PASS	12	9	22.25	1.62	1.62	BLVRB	19q13.1-q13.2	biliverdin reductase B (flavin reductase (NADPH))
K147_ADCY	D63481_at	D63481	PASS	7	9.57	PASS	12	7	5.92	1.62	1.62	KIAA0147		The KIAA0147 gene product is related to adenyl cyclase.
K115_OLIG1	D29643_at	D29643	PASS	9	26.22	PASS	13	9	16.23	1.62	1.62	KIAA0115		similar to Canis oligosaccharyltransferase 48 kDa subunit (M98392)
RPL11	X79234_at	X79234	PASS	9	299.56	PASS	13	9	185.62	1.61	1.61	RPL11	1	ribosomal protein L11

# Protein Family

HNRPA2B1	M29064_at	M29064	PASS	9	34.00	PASS	13	9	21.08	1.61	1.61	1.61	HNRPA2B1	7p15	heterogeneous nuclear ribonucleoprotein A2/B1	heterogeneous nuclear ribonucleoprotein A2/B1
PSM27	AB003177_a	AB003177	PASS	7	16.71	PASS	11	7	10.36	1.61	1.61	1.61	PSMD9	12q24.31-q24.32	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9
D42040_s at	D42040_s at	D42040	PASS	8	20.38	PASS	11	8	12.64	1.61	1.61	1.61	KIAA9001	11q13.3	aryl hydrocarbon receptor-interacting protein	KIAA9001 gene product
ARA9	U78521_at	U78521	PASS	9	54.56	PASS	13	9	33.85	1.61	1.61	1.61	AIP		aryl hydrocarbon receptor-interacting protein	aryl hydrocarbon receptor-interacting protein
K245_PRMA	D87432_at	D87432	PASS	8	7.88	PASS	9	8	4.89	1.61	1.61	1.61	SLC7A6		solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6
GMFB	AB001106_a	AB001106	PASS	7	10.14	PASS	13	7	6.31	1.61	1.61	1.61	GMFB		glya maturation factor, beta	glya maturation factor, beta
K136	D50926_at	D50926	PASS	8	11.50	PASS	13	8	7.15	1.61	1.61	1.61	KIAA0136		novel	The KIAA0136 gene product is novel.
BM11	L13689_at	L13689	PASS	9	9.89	PASS	13	9	6.15	1.61	1.61	1.61	BM11	10p13	murine leukemia viral (bmi-1) oncogene homolog	murine leukemia viral (bmi-1) oncogene homolog
MVK	L77213_at	L77213	PASS	6	8.83	PASS	10	6	5.50	1.61	1.61	1.61			phosphomevalonate kinase	phosphomevalonate kinase
PNN	U77718_at	U77718	PASS	8	10.50	PASS	13	8	6.54	1.61	1.61	1.61	PNN		pinin, desmosome associated protein	pinin, desmosome associated protein
I3KDDAP	U34343_at	U34343	PASS	9	27.67	PASS	13	9	17.23	1.61	1.61	1.61			13kD differentiation-associated protein	13kD differentiation-associated protein
AF000424_s	AF000424_s	AF000424	PASS	8	58.25	PASS	13	8	42.54	1.60	1.60	1.60	LST1		putative DNA dependent ATPase and helicase	putative DNA dependent ATPase and helicase
U72936_s at	U72936_s at	U72936	PASS	8	9.38	PASS	13	8	5.85	1.60	1.60	1.60	ATRX		transducin beta-2 subunit	XH2; XNP; alternatively spliced product 1; contains all exons; translation starts in exon 9; ATRX gene deposited in GenBank Accession Numbers U72900-U72935
M36429_s at	M36429_s at	M36429	PASS	7	15.29	PASS	13	7	9.34	1.60	1.60	1.60	EEF1B2	2	eukaryotic translation elongation factor 1 beta 2	eukaryotic translation elongation factor 1 beta 2
EEF1B1	X60489_at	X60489	PASS	9	134.56	PASS	13	9	84.00	1.60	1.60	1.60			capping protein alpha subunit isoform 1	
CAPZA	U56637_at	U56637	PASS	9	62.33	PASS	13	9	38.92	1.60	1.60	1.60			ribosomal protein L28	ribosomal protein L28
RPL28	U14969_at	U14969	PASS	9	444.22	PASS	13	9	277.62	1.60	1.60	1.60	DVL3	19q13.4-3q27	dishevelled 3 (homologous to Drosophila dsh)	dishevelled 3 (homologous to Drosophila dsh)
K208_DISH1	D86963_at	D86963	PASS	6	9.33	PASS	12	6	5.83	1.60	1.60	1.60	COL11A1	1p21	collagen, type XI, alpha 1	collagen, type XI, alpha 1
COL11A1	J04177_at	J04177	PASS	6	7.00	PASS	8	6	4.38	1.60	1.60	1.60	D123		D123 gene product	D123 gene product
PD123	D14878_at	D14878	PASS	8	10.13	PASS	12	8	6.33	1.60	1.60	1.60	KIAA0063		KIAA0063 gene product	KIAA0063 gene product
K63	D31884_at	D31884	PASS	9	11.33	PASS	11	9	7.09	1.60	1.60	1.60	ATP5G2	12	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2
ATP5G2_ma	X69908_ma	X69908	PASS	9	48.67	PASS	13	9	30.46	1.60	1.60	1.60			chitinase 3-like 2	chitinase 3-like 2
PAP	X76770_at	X76770	PASS	7	10.14	PASS	11	7	6.36	1.59	1.59	1.59	CHI3L2	1p13.3	YKL-39 precursor	YKL-39 precursor
U49835_s at	U49835_s at	U49835	PASS	9	13.67	PASS	12	9	8.58	1.59	1.59	1.59	CDIC10		cell division cycle 10 (homologous to CDC10 of S. cerevisiae)	cell division cycle 10 (homologous to CDC10 of S. cerevisiae)
CDIC10	S72008_at	S72008	PASS	9	32.33	PASS	13	9	20.31	1.59	1.59	1.59				

IQGAP1	L33075_at	L33075	PASS	9	42.00	PASS	13	9	26.38	1.59	1.59	1.59	IQGAP1		ras GTPase-activating-like protein	amino acid feature: IQ calmodulin-binding domains, aa 740 .. 865; amino acid feature: N-terminal repeats, aa 210 .. 680; amino acid feature: Sar1 homologous region, aa 920 .. 1657; amino acid feature: putative GAP catalytic domain, aa 1000 .. 1270
IMPDH2_ma	L33842_ma	L33842	PASS	9	15.89	PASS	13	9	10.00	1.59	1.59	1.59	IMPDH2	3p21.2	IMP (inosine monophosphate) dehydrogenase 2	IMP (inosine monophosphate) dehydrogenase 2
RAND	D25274_at	D25274	PASS	9	26.33	PASS	13	9	16.62	1.58	1.58	1.58			G protein pathway suppressor 1	G protein pathway suppressor 1
GPS1	U20285_at	U20285	PASS	9	15.11	PASS	13	9	9.54	1.58	1.58	1.58	GPS1			
LYZ_f	J03801_f	J03801	PASS	9	176.33	PASS	13	9	111.31	1.58	1.58	1.58	LYZ	12	lysozyme	lysozyme (renal amyloidosis)
SRD5A1	M32313_at	M32313	PASS	7	8.14	PASS	7	7	5.14	1.58	1.58	1.58	SRD5A1	5p15	steroid-5-alpha-reductase, alpha polypeptide 1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5-alpha-steroid delta 4-dehydrogenase alpha 1)
RPS24L	M81757_at	M81757	PASS	9	420.33	PASS	13	9	265.54	1.58	1.58	1.58	RPS19	19q13.2	ribosomal protein S19	ribosomal protein S19
ARC20	AF006087_at	AF006087	PASS	8	19.63	PASS	10	8	12.40	1.58	1.58	1.58	ARC20		20 kD subunit of the Arp2/3 protein complex	20 kD subunit of the Arp2/3 protein complex
ARHA	L25080_at	L25080	PASS	9	143.56	PASS	13	9	90.77	1.58	1.58	1.58	ARHA	3p21.3	GTP-binding protein	ras homolog gene family, member A
RPLP1	M17886_at	M17886	PASS	9	381.67	PASS	13	9	241.38	1.58	1.58	1.58	RPLP1		ribosomal protein, large, P1	ribosomal protein, large, P1
PRKAR2B	M31158_at	M31158	PASS	8	17.75	PASS	13	8	11.23	1.58	1.58	1.58	PRKAR2B	7q31-qter	protein kinase, cAMP-dependent, regulatory, type II, beta	protein kinase, cAMP-dependent, regulatory, type II, beta
BAG1	Z35491_at	Z35491	PASS	8	9.63	PASS	11	8	6.09	1.58	1.58	1.58	BAG1	9p12	BCL2-associated athanogene	BCL2-associated athanogene
RPS20	HG1800-HT	HG1800-HT	PASS	9	384.89	PASS	13	9	243.62	1.58	1.58	1.58				
L43575_s	at L43575_s	at L43575	PASS	8	10.63	PASS	11	8	6.73	1.58	1.58	1.58				
CHS1	U67615_at	U67615	PASS	7	10.00	PASS	12	7	6.33	1.58	1.58	1.58	CHS1	1q42.1-q42.2	Chediak-Higashi syndrome 1	Chediak-Higashi syndrome 1
RAP1A	M22995_at	M22995	PASS	8	16.13	PASS	13	8	10.23	1.58	1.58	1.58	RAP1A	1p13.3	RAP1A, member of RAS oncogene family	RAP1A, member of RAS oncogene family
L04483_s	at L04483_s	at L04483	PASS	9	437.33	PASS	13	9	277.77	1.57	1.57	1.57	RPS21	20q13.3	ribosomal protein S21	ribosomal protein S21
KSRP	U94832_at	U94832	PASS	9	8.44	PASS	11	9	5.36	1.57	1.57	1.57			KSRP	RNA binding protein; KH type RNA binding domain; alternative splicing regulator; cooperative complex formation
PSMB6	D29012_at	D29012	PASS	9	24.44	PASS	13	9	15.54	1.57	1.57	1.57	PSMB6	17p13	proteasome subunit Y	proteasome (prosome, macropain) subunit, beta type, 6
RLIP76	L42542_at	L42542	PASS	8	11.25	PASS	13	8	7.15	1.57	1.57	1.57			RLIP76 protein	
LMO2_ma	X61118_ma	X61118	PASS	8	15.00	PASS	13	8	9.54	1.57	1.57	1.57	TTG-2a/RBTN-2a			
BPGM	X04327_at	X04327	PASS	7	7.86	PASS	11	7	5.00	1.57	1.57	1.57	BPGM	7q31-q34	2,3-bisphosphoglycerate mutase	2,3-bisphosphoglycerate mutase
MTHFD	J04031_at	J04031	PASS	7	7.86	PASS	8	7	5.00	1.57	1.57	1.57	MTHFD	14q24		5,10-methylenetetrahydrofolate dehydrogenase, 5,10-methylenetetrahydrofolate cyclohydrolase, 10-formyltetrahydrofolate synthetase

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23KDRP	X56932_at	X56932	PASS	9	454.22	PASS	13	9	289.23	1.57	1.57	1.57	23 kD highly basic protein	
RPL17	X57959_at	X57959	PASS	9	127.33	PASS	13	9	81.15	1.57	1.57	1.57	ribosomal protein L7	
RPS14_cd82	M13934_cd5	M13934	PASS	9	368.11	PASS	13	9	235.08	1.57	1.57	1.57	unknown protein	8
ESD	M13450_at	M13450	PASS	8	19.88	PASS	13	8	12.69	1.57	1.57	1.57	13q14.1-q14.2	
LDLR	L00352_at	L00352	PASS	5	8.00	PASS	9	5	5.11	1.57	1.57	1.57	low density lipoprotein receptor (familial hypercholesterolemia)	19p13.3
E_23612	U90902_at	U90902	PASS	9	11.33	PASS	12	9	7.25	1.56	1.56	1.56		
ADD1SP2	HG651-HT42	HG651-HT	PASS	9	20.89	PASS	13	9	13.38	1.56	1.56	1.56		
SEC61B	L25083_at	L25083	PASS	9	28.44	PASS	13	9	18.23	1.56	1.56	1.56	Sec61-complex beta-subunit	
U2AF1	M96982_at	M96982	PASS	9	28.56	PASS	13	9	18.31	1.56	1.56	1.56	U2 snRNP auxiliary factor	
HLA-DRB5	M33600_f_a	M33600	PASS	9	171.78	PASS	13	9	110.15	1.56	1.56	1.56	major histocompatibility complex, class II, DR beta 5	6p21.3
XPC	D21089_at	D21089	PASS	7	17.29	PASS	11	7	11.09	1.56	1.56	1.56	xeroderma pigmentosum, complementation group C	3p25
BCL2L1	Z23115_at	Z23115	PASS	8	10.13	PASS	8	8	6.50	1.56	1.56	1.56	BCL2-like 1	
AT1C	D82348_at	D82348	PASS	9	15.33	PASS	13	9	9.85	1.56	1.56	1.56	5-aminimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	
DNMTN	U50733_at	U50733	PASS	9	15.56	PASS	13	9	10.00	1.56	1.56	1.56	dynamitin	
GBP2	M55543_at	M55543	PASS	9	12.44	PASS	11	9	8.00	1.56	1.56	1.56	guanylate binding protein 2, interferon-inducible	
RPS12	HG613-HT6	HG613-HT	PASS	9	290.33	PASS	13	9	186.69	1.56	1.56	1.56		
DNCL12	U32944_at	U32944	PASS	9	42.67	PASS	13	9	27.46	1.55	1.55	1.55		
CTCF	U25435_at	U25435	PASS	7	8.29	PASS	12	7	5.33	1.55	1.55	1.55	CTCF	14q24
GATA3	X58072_at	X58072	PASS	7	8.29	PASS	12	7	5.33	1.55	1.55	1.55	IGATA3 transcription factor	
TRIP3	L40410_at	L40410	PASS	9	11.00	PASS	12	9	7.08	1.55	1.55	1.55	thyroid receptor interactor 3	
FIP1	U41654_at	U41654	PASS	9	11.22	PASS	13	9	7.23	1.55	1.55	1.55	adenovirus E3-14.7K interacting protein 1	
L25931_s_at	L25931_s_at	L25931	PASS	9	15.78	PASS	12	9	10.17	1.55	1.55	1.55	lamin B receptor	1q42.1
TFE3_mal	X97160_mal	X97160	PASS	7	9.29	PASS	7	7	6.00	1.55	1.55	1.55	TFE3 transcription factor	
CYP1B1	U03688_at	U03688	PASS	5	8.40	PASS	7	5	5.43	1.55	1.55	1.55	cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile)	2p21
K118_RAB8	D42087_at	D42087	PASS	9	9.00	PASS	11	9	5.82	1.55	1.55	1.55	The gene product of HA0793 is related to Dictyostelium discoideum RabB protein.	
LDHB_mal	X13794_mal	X13794	PASS	9	69.00	PASS	13	9	44.62	1.55	1.55	1.55	lactate dehydrogenase B	
E51	L37368_at	L37368	PASS	8	14.75	PASS	13	8	9.54	1.55	1.55	1.55	RNA-binding protein	
U04285_s_at	U04285_s_at	U04285	PASS	6	14.50	PASS	13	6	9.38	1.55	1.55	1.55	lysosomal acid lipase/cholesteryl ester hydrolase	
QDPR	M16447_at	M16447	PASS	7	7.14	PASS	8	7	4.63	1.54	1.54	1.54	quinoid dihydropteridine reductase	4p15.3



# Table 3

ATP5	M37104_at	M37104	PASS	9	11.44	PASS	12	9	7.42	1.54	1.54	ATP5	10	ATP synthase, H <sup>+</sup> transporting, mitochondrial
ATP6E	D49400_at	D49400	PASS	9	33.11	PASS	13	9	21.46	1.54	1.54	ATP6S14	12	ATPase, vacuolar, 14 kD
TISI1D	U07802_at	U07802	PASS	9	37.56	PASS	13	9	24.38	1.54	1.54	TISI1d		similar to human PHAPI2a encoded by GenBank Accession Number Y07569 and human PHAPI2b encoded by GenBank Accession Number Y07570
U70439_s_at	U70439_s_at	U70439	PASS	9	87.67	PASS	13	9	56.92	1.54	1.54			cold inducible RNA-binding protein
CIRBP	D78134_at	D78134	PASS	9	53.89	PASS	13	9	35.00	1.54	1.54	CIRBP		mad protein homolog
MAD2L1	U68018_at	U68018	PASS	7	9.00	PASS	13	7	5.85	1.54	1.54	hMAD-2		ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)
RPL30	HG2873-HT	HG2873-H	PASS	9	487.44	PASS	13	9	317.15	1.54	1.54	ATP50	21q22.1-q22.2	match to X98253 (NID:q2274981) (PID:q2274982)
ATP50	X83218_at	X83218	PASS	9	22.44	PASS	13	9	14.62	1.54	1.54			UbcH10
RPL26	HG384-HT3	HG384-HT	PASS	9	170.56	PASS	13	9	111.08	1.54	1.54			2,4-dienoyl CoA reductase
AC002477_s	AC002477_s	AC002477	PASS	9	13.22	PASS	13	9	8.62	1.53	1.53	ZNF183		GATA-binding protein 3
UBECS	U73379_at	U73379	PASS	5	9.20	PASS	10	5	6.00	1.53	1.53			interleukin 8 receptor, beta
DECR	U49352_at	U49352	PASS	6	10.17	PASS	11	6	6.64	1.53	1.53	DECR	8q21.3	TAF1155
X55037_s_at	X55037_s_at	X55037	PASS	7	9.86	PASS	9	7	6.44	1.53	1.53	GATA3	10p15	diaprepam binding inhibitor
IL8RB	L19593_at	L19593	PASS	5	7.80	PASS	10	5	5.10	1.53	1.53	IL8RB	2q35	aconitase 2, mitochondrial
TAF2D	U18062_at	U18062	PASS	9	8.67	PASS	12	9	5.67	1.53	1.53	TAF155		HLA-E
DBI	M14200_ma	M14200	PASS	8	16.00	PASS	13	8	10.46	1.53	1.53	DBI		neutrophil lipocalin
HG4264-HT4	HG4264-HT	HG4264-H	PASS	9	14.11	PASS	13	9	9.23	1.53	1.53			myeloid cell nuclear differentiation antigen
ACO2	U80040_at	U80040	PASS	8	13.75	PASS	13	8	9.00	1.53	1.53	ACO2	22q11.2-q13.1	T-cell receptor, beta cluster
HLAE	X56841_at	X56841	PASS	9	140.78	PASS	13	9	92.31	1.53	1.53	HLA-E		amyloid beta (A4) precursor-like protein 2
NEFTS	HG3236-HT3	HG3236-H	PASS	9	44.22	PASS	13	9	29.00	1.52	1.52			ferritin, light polypeptide
ACAT1	HG4073-HT4	HG4073-H	PASS	9	9.78	PASS	12	9	6.42	1.52	1.52			protein phosphatase 1, regulatory (inhibitor) subunit 8
S75256_s_at	S75256_s_at	S75256	PASS	8	10.25	PASS	11	8	6.73	1.52	1.52	HN1		calmodulin
MNDA	M81750_at	M81750	PASS	8	41.13	PASS	13	8	27.00	1.52	1.52	MNDA	1q22	casein kinase 2, beta polypeptide
TCRB	M12886_at	M12886	PASS	9	227.67	PASS	13	9	149.69	1.52	1.52	TCRB	7q35	la-associated gamma chain
L09209_s_at	L09209_s_at	L09209	PASS	9	45.89	PASS	13	9	30.23	1.52	1.52	APLP2	11q23-q25	ribosomal protein L38
FTL	M11147_at	M11147	PASS	9	409.56	PASS	13	9	269.92	1.52	1.52	FTL	19q13.3-q13.4	chloride intracellular channel 1
ARD1	U14575_at	U14575	PASS	8	8.25	PASS	9	8	5.44	1.52	1.52	PP1R8	Chr.1	non-histone chromosomal protein
HLA-A	M94880_f	M94880	PASS	9	275.11	PASS	13	9	181.69	1.51	1.51			
M19311_s_at	M19311_s_at	M19311	PASS	9	108.67	PASS	13	9	71.77	1.51	1.51			
M30448_s_at	M30448_s_at	M30448	PASS	9	58.11	PASS	13	9	38.38	1.51	1.51	CSNK2B	6p21-p12	
BACTIN3	AFEX-HSAC	AFEX-HS	PASS	9	385.33	PASS	13	9	254.54	1.51	1.51			
M13560_s_at	M13560_s_at	M13560	PASS	9	150.33	PASS	13	9	99.31	1.51	1.51			
RBL38	Z26876_at	Z26876	PASS	9	308.11	PASS	13	9	203.62	1.51	1.51	RPL38	17	
CLIC1	U91205_at	U91205	PASS	9	94.22	PASS	13	9	62.31	1.51	1.51	CLIC1		
NHC	U90549_at	U90549	PASS	5	12.40	PASS	10	5	8.20	1.51	1.51	NHC		

# Table 300

NPAT	D83243_at	D83243	PASS	9	9.89	PASS	11	9	6.55	1.51	1.51	NPAT	11q22-q23	nuclear protein, ataxia-telangiectasia locus	nuclear protein, ataxia-telangiectasia locus
NRNPC	M16342_at	M16342	PASS	9	25.44	PASS	13	9	16.85	1.51	1.51	HNRPC		heterogeneous nuclear ribonucleoprotein C (C1/C2)	heterogeneous nuclear ribonucleoprotein C (C1/C2)
HGI1322-IT1	HGI1322-IT1	HGI1322-IT1	PASS	9	49.22	PASS	13	9	32.62	1.51	1.51				
SNCA	U46901_at	U46901	PASS	9	8.11	PASS	8	9	5.38	1.51	1.51	SNCA	4q21.3-q22	synuclein, alpha (non A4 component of amyloid precursor)	synuclein, alpha (non A4 component of amyloid precursor)
K5	D13630_at	D13630	PASS	8	12.75	PASS	11	8	8.45	1.51	1.51	KIAA0005		KIAA0005 gene product	KIAA0005 gene product
HDA1C	D50405_at	D50405	PASS	9	16.22	PASS	13	9	10.77	1.51	1.51	HDA1C	1p34.1	histone deacetylase 1	histone deacetylase 1
GJA4	Y08915_at	Y08915	PASS	9	19.11	PASS	13	9	12.69	1.51	1.51	IGBP1	Xq13.1-q13.3	immunoglobulin (CD79A) binding protein 1	immunoglobulin (CD79A) binding protein 1
LUCAL15	U23946_at	U23946	PASS	6	9.33	PASS	10	6	6.20	1.51	1.51	LUCAL15		putative tumor suppressor	putative tumor suppressor
VDAC2	L08666_at	L08666	PASS	9	19.89	PASS	13	9	13.23	1.50	1.50	VDAC2	10q22	voltage-dependent anion channel 2	voltage-dependent anion channel 2
M83667_ma	M83667_ma	M83667	PASS	9	42.67	PASS	13	9	28.38	1.50	1.50	NF-IL6-beta		NF-IL6-beta protein	NF-IL6-beta protein
C113	U57877_at	U57877	PASS	5	14.80	PASS	13	5	9.85	1.50	1.50	SDHC	1q21	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD
U89922_s_at	U89922_s_at	U89922	PASS	9	143.56	PASS	13	9	95.54	1.50	1.50	LTB	6p21.3	lymphotoxin beta (TNF superfamily, member 3)	lymphotoxin beta (TNF superfamily, member 3)
LYZ_ma1_f	X14008_ma1_f	X14008	PASS	9	159.22	PASS	13	9	106.00	1.50	1.50			lysosome	Protein sequence is in conflict with the conceptual translation.
NDUFV2	M22538_at	M22538	PASS	8	28.88	PASS	13	8	19.23	1.50	1.50	NDUFV2	18p11.31-p11.2	NADH-ubiquinone reductase (ubiquinone) flavoprotein 2 (24kD)	NADH-ubiquinone reductase (ubiquinone) flavoprotein 2 (24kD)
L05072_s_at	L05072_s_at	L05072	PASS	9	17.56	PASS	13	9	11.69	1.50	1.50	IRF1	5q23-q31	interferon regulatory factor 1	interferon regulatory factor 1
K247	D87434_at	D87434	PASS	8	10.63	PASS	13	8	7.08	1.50	1.50	KIAA0247		KIAA0247 gene product	KIAA0247 gene product
RPS10	U14972_at	U14972	PASS	9	350.00	PASS	13	9	233.31	1.50	1.50	RPS10	6	ribosomal protein S10	ribosomal protein S10
NOT56L	Y09022_at	Y09022	PASS	8	12.13	PASS	12	8	8.08	1.50	1.50	not		Not56-like protein	Not56-like protein
BTG1	X61123_at	X61123	PASS	9	54.11	PASS	13	9	36.08	1.50	1.50	BTG1	12q22	B-cell translocation gene 1, anti-proliferative	B-cell translocation gene 1, anti-proliferative
HMOX1	X06985_at	X06985	PASS	8	32.63	PASS	13	8	21.77	1.50	1.50	HMOX1	22q12	heme oxygenase (decycling) 1	heme oxygenase (decycling) 1
RPS29	U14973_at	U14973	PASS	9	390.44	PASS	13	9	260.54	1.50	1.50	RPS29	14	ribosomal protein S29	ribosomal protein S29
PSMHSC7	D26599_at	D26599	PASS	9	24.22	PASS	12	9	16.17	1.50	1.50	PSMB2	1p34.2	proteasome (prosome, macropain) subunit, beta type, 2	proteasome (prosome, macropain) subunit, beta type, 2
SPTBN1	M96803_at	M96803	PASS	5	10.60	PASS	13	5	7.08	1.50	1.50	SPTBN1	2p21	spectrin, beta, non-erythrocytic 1	spectrin, beta, non-erythrocytic 1
K98_TCP1	D43950_at	D43950	PASS	8	17.63	PASS	13	8	11.77	1.50	1.50	KIAA0098		KIAA0098 is a human counterpart of mouse chaperonin containing TCP-1 gene.	KIAA0098 is a human counterpart of mouse chaperonin containing TCP-1 gene.
K137_COSC	D50927_at	D50927	PASS	8	10.25	PASS	13	8	6.85	1.50	1.50	KIAA0137		KIAA0137 gene product	KIAA0137 gene product
PAK1	U24152_at	U24152	PASS	9	13.22	PASS	12	9	8.83	1.50	1.50	PAK1	11q13-q14	p21/Cdc42/Rac1-activated kinase 1 (yeast Ste20-related)	p21/Cdc42/Rac1-activated kinase 1 (yeast Ste20-related)
U76764_s_at	U76764_s_at	U76764	PASS	9	38.67	PASS	13	9	25.85	1.50	1.50	CD97	19p13	CD97 antigen	CD97 antigen
X65965_s_at	X65965_s_at	X65965	PASS	9	19.44	PASS	13	9	13.00	1.50	1.50				

HCpA78L	S73591_at	S73591	PASS	9	350.56	PASS	13	9	234.46	1.50	1.50	brain-expressed HHCPA78 homolog	VDUP1	1.25-dihydroxyvitamin D-3 up-regulated; This sequence comes from Fig. 2. Protein sequence is in conflict with the conceptual translation; mismatch(26(K-&gt;R))
S79873_s_at	S79873_s_at	S79873	PASS	7	7.29	PASS	8	7	4.88	1.49	1.49	LAMP2	lysosomal-associated membrane protein 2	lysosomal-associated membrane protein 2
L03411_s_at	L03411_s_at	L03411	PASS	9	10.00	PASS	13	9	6.69	1.49	1.49	RD	Radin blood group	Radin blood group
R7527	HG3214-HT1	HG3214-H	PASS	9	438.11	PASS	13	9	293.46	1.49	1.49	COX8	cytochrome c oxidase subunit VIII	cytochrome c oxidase subunit VIII
COX8_ma1	J04823_ma1	J04823	PASS	9	80.33	PASS	13	9	53.85	1.49	1.49	COX8	cytochrome c oxidase subunit VIII	cytochrome c oxidase subunit VIII
K127	D50917_at	D50917	PASS	7	8.29	PASS	9	7	5.56	1.49	1.49	KIAA0127	KIAA0127 gene product	KIAA0127 gene product
M36284_s_a	M36284_s_a	M36284	PASS	9	28.33	PASS	13	9	19.00	1.49	1.49	GYPC	glycophorin C (Gerbich blood group)	glycophorin C (Gerbich blood group)
NOF1	U39400_at	U39400	PASS	8	11.25	PASS	11	8	7.55	1.49	1.49	C11orf4	chromosome 11 open reading frame 4	chromosome 11 open reading frame 4
WTRP	HG3549-HT1	HG3549-H	PASS	9	410.22	PASS	13	9	275.23	1.49	1.49			
NELRP2	D83018_at	D83018	PASS	9	18.22	PASS	13	9	12.23	1.49	1.49	PSMD11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11
PSM445	AB003102_a	AB003102	PASS	7	13.57	PASS	9	7	9.11	1.49	1.49			
UDPPH	U27460_at	U27460	PASS	9	12.22	PASS	9	9	8.22	1.49	1.49			similar to uridine diphosphoglucose pyrophosphorylase in human liver, Swiss-Prot Accession Number Q07131; the 5'UTR and 3'UTR of this clone are completely different from those of the liver form
DF570	U94319_at	U94319	PASS	9	12.00	PASS	13	9	8.08	1.49	1.49	P52/P75	transcriptional coactivator p52/p75	transcriptional coactivator p52/p75
HRG4	U40998_at	U40998	PASS	8	11.75	PASS	12	8	7.92	1.48	1.48	UNC119	unc119 (C.elegans) homolog	unc119 (C.elegans) homolog
P43LSB	S75463_at	S75463	PASS	9	29.11	PASS	13	9	19.62	1.48	1.48	TUFM	Tu translation elongation factor, mitochondrial	Tu translation elongation factor, mitochondrial
RPL18AH	L11566_at	L11566	PASS	9	309.00	PASS	13	9	208.23	1.48	1.48	RPL18	ribosomal protein L18	ribosomal protein L18
ATPA	D14710_at	D14710	PASS	9	90.22	PASS	13	9	60.85	1.48	1.48	ATP5A1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle
K261_SIS	D87450_at	D87450	PASS	9	8.67	PASS	13	9	5.85	1.48	1.48	KIAA0261	Similar to D.melanogaster parallel sister chromatids protein	Similar to D.melanogaster parallel sister chromatids protein
HBC647	U68494_at	U68494	PASS	7	8.00	PASS	10	7	5.40	1.48	1.48			
OAZ	D78361_at	D78361	PASS	9	383.22	PASS	13	9	238.69	1.48	1.48	RPL32	ribosomal protein L32	ribosomal protein L32
RPL32	X03342_at	X03342	PASS	9	420.11	PASS	13	9	283.85	1.48	1.48	RPL32	ribosomal protein L32	ribosomal protein L32
U19247_ma1	U19247_ma1	U19247	PASS	9	14.11	PASS	13	9	9.54	1.48	1.48	IFNGR1	interferon gamma receptor 1	interferon gamma receptor 1
SATB1	M97287_at	M97287	PASS	9	19.78	PASS	13	9	13.38	1.48	1.48	SATB1	special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's)	special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's)
CIT987SK_r	U96629_ma2	U96629	PASS	8	8.13	PASS	8	8	5.50	1.48	1.48	2A8.2	unknown protein	unknown protein
HG1471-HT1	HG1471-HT1	HG1471-H	PASS	7	7.71	PASS	9	7	5.22	1.48	1.48	CIT987SK_2A8_1		

# Table 1

CD48	M3766_at	M3766	PASS	9	121.67	PASS	13	9	82.38	1.48	1.48	CD48	1q21.3-q22	CD48 antigen (B-cell membrane protein)	CD48 antigen (B-cell membrane protein)
HNRPA1	m12671	m12671	PASS	9	87.11	PASS	13	9	59.00	1.48	1.48	UBE2N		ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)	ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)
UBE2N	D83004_at	D83004	PASS	9	9.89	PASS	10	9	6.70	1.48	1.48	GTF2A1		general transcription factor IIA, 1 (37kD and 19kD subunits)	general transcription factor IIA, 1 (37kD and 19kD subunits)
GTF2A2	U14193_at	U14193	PASS	8	11.13	PASS	13	8	7.54	1.48	1.48	UGT1		highly similar to UDP-N-acetylglucosamine transporter of K. lactis	highly similar to UDP-N-acetylglucosamine transporter of K. lactis
T1227H	D50325_at	D50325	PASS	9	9.44	PASS	10	9	6.40	1.48	1.48	SAP145		glycosome associated protein	glycosome associated protein
UGALT	D87989_at	D87989	PASS	7	13.14	PASS	11	7	8.91	1.48	1.48	CX3CR1	3p21	chemokine (C-X3-C) receptor 1	chemokine (C-X3-C) receptor 1
SAP145	U141371_at	U141371	PASS	9	17.78	PASS	11	9	12.09	1.47	1.47	RPL27	17	ribosomal protein L27	ribosomal protein L27
CMRRL1	U20350_at	U20350	PASS	9	63.78	PASS	13	9	43.38	1.47	1.47	SPTAN1	9q33-q34	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)
RPL27	L19527_at	L19527	PASS	9	320.89	PASS	13	9	218.31	1.47	1.47	Ku		Ku (p70/p80) subunit	Ku (p70/p80) subunit
SPTAN1	J05243_at	J05243	PASS	8	8.00	PASS	9	8	5.44	1.47	1.47	KIAA0111		signal recognition particle 14kD (homologous Alu RNA-binding protein)	signal recognition particle 14kD (homologous Alu RNA-binding protein)
G22P1	M30938_at	M30938	PASS	9	19.78	PASS	13	9	13.46	1.47	1.47	KIAA0111		interferon-induced protein 17	interferon-induced protein 17
MCP	X59405_at	X59405	PASS	8	9.38	PASS	13	8	6.38	1.47	1.47	IFIT1		interferon-induced protein 17	interferon-induced protein 17
K264	D87453_at	D87453	PASS	5	7.60	PASS	11	5	5.18	1.47	1.47	CCT6		chaperonin containing T-complex subunit 6	chaperonin containing T-complex subunit 6
SRP14	U07857_at	U07857	PASS	9	47.78	PASS	13	9	32.62	1.46	1.46	NPCL1		Niemann-Pick disease, type C1	Niemann-Pick disease, type C1
K111	NUK3	D21853_at	PASS	9	16.00	PASS	13	9	10.92	1.46	1.46	HSPF1		heat shock protein 40	heat shock protein 40
IFIT2/SEP	J04164_at	J04164	PASS	9	227.56	PASS	13	9	155.38	1.46	1.46	calneurin A catalytic subunit		calneurin A catalytic subunit	calneurin A catalytic subunit
RPL35	U12465_at	U12465	PASS	9	268.44	PASS	13	9	183.31	1.46	1.46	calmodulin-dependent protein phosphatase catalytic subunit		calmodulin-dependent protein phosphatase catalytic subunit	calmodulin-dependent protein phosphatase catalytic subunit
CCT6	L27706_at	L27706	PASS	7	9.57	PASS	13	7	6.54	1.46	1.46	CaM-P-PP		CaM-P-PP	CaM-P-PP
FNTA	L10413_at	L10413	PASS	9	34.33	PASS	13	9	23.46	1.46	1.46	CaM-P-PP		CaM-P-PP	CaM-P-PP
RPS9	U14971_at	U14971	PASS	9	277.78	PASS	13	9	189.85	1.46	1.46	CaM-P-PP		CaM-P-PP	CaM-P-PP
U09510 s at	U09510 s at	U09510 s at	PASS	9	8.33	PASS	10	9	5.70	1.46	1.46	CaM-P-PP		CaM-P-PP	CaM-P-PP
PECAM1	L34657_at	L34657	PASS	8	18.75	PASS	12	8	12.83	1.46	1.46	CaM-P-PP		CaM-P-PP	CaM-P-PP
NPCL1	AF002020 at	AF002020 at	PASS	5	8.60	PASS	9	5	5.89	1.46	1.46	CaM-P-PP		CaM-P-PP	CaM-P-PP
HSP40	D85429_at	D85429	PASS	9	21.89	PASS	13	9	15.00	1.46	1.46	CaM-P-PP		CaM-P-PP	CaM-P-PP
PPP3CB	S46622_at	S46622	PASS	5	6.40	PASS	10	5	4.40	1.45	1.45	CaM-P-PP		CaM-P-PP	CaM-P-PP
ZPK	U07358 at	U07358	PASS	7	8.86	PASS	11	7	6.09	1.45	1.45	CaM-P-PP		CaM-P-PP	CaM-P-PP
RPL12	L06505 at	L06505	PASS	9	221.67	PASS	13	9	152.46	1.45	1.45	CaM-P-PP		CaM-P-PP	CaM-P-PP
MMP1	M63483 at	M63483	PASS	5	12.60	PASS	12	5	8.67	1.45	1.45	CaM-P-PP		CaM-P-PP	CaM-P-PP



# Table 1

CD79B	M89957_at	M89957	PASS	6	12.33	PASS	11	6	8.64	1.43	1.43	CD79B	17q23	cell surface glycoprotein	CD79B antigen (immunoglobulin-associated beta)
UQCRLF1	L32977_at	L32977	PASS	9	27.22	PASS	13	9	19.08	1.43	1.43	UQCRLF1		Rieske Fe-S protein	phosphate carrier, mitochondrial
PHC	X60036_at	X60036	PASS	9	57.89	PASS	13	9	40.62	1.43	1.43	PHC	12	phosphate carrier, mitochondrial	phosphate carrier, mitochondrial
RPS16	M60854_at	M60854	PASS	9	411.67	PASS	13	9	289.15	1.42	1.42	RPS16	19q	ribosomal protein S16	ribosomal protein S16
TMSB4	M17733_at	M17733	PASS	9	430.44	PASS	13	9	302.69	1.42	1.42	TMSB4	Y	thymosin, beta 4, Y chromosome	thymosin, beta 4, Y chromosome
HMGCL	L07033_at	L07033	PASS	8	7.75	PASS	11	8	5.45	1.42	1.42	HMGCL	1	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaryl-CoA lyase)	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaryl-CoA lyase)
RPS6KA2	U08316_at	U08316	PASS	5	8.00	PASS	11	5	5.64	1.42	1.42	RPS6KA3	Xp22.2-p22.1	ribosomal protein S6 kinase, 90kD, polypeptide 3	ribosomal protein S6 kinase, 90kD, polypeptide 3
M96995_s_at	M96995_s_at	M96995	PASS	6	18.00	PASS	13	6	12.69	1.42	1.42	GRB2	17q24-q25	growth factor receptor-bound protein 2	growth factor receptor-bound protein 2
U43901_ma	U43901_ma	U43901	PASS	9	287.89	PASS	13	9	203.08	1.42	1.42			37 kD laminin receptor precursor/p40 ribosome associated protein	37LR/p40, metastasis-associated multifunctional protein
RPL37A	L06499_at	L06499	PASS	9	428.44	PASS	13	9	302.38	1.42	1.42	RPL37A		ribosomal protein L37a	ribosomal protein L37a
GLB1	M83822_at	M83822	PASS	7	7.43	PASS	12	7	5.25	1.41	1.41	BGL		beige-like protein	similar to yeast YCR032w, GenBank Accession Number X59720, Mus musculus BG, GenBank Accession Number U52461 and C. elegans F10F2.1, GenBank Accession Number Z35598; previously identified as CDC4L
F13A1	M14539_at	M14539	PASS	9	78.00	PASS	13	9	55.15	1.41	1.41	F13A1	6p24.2-p23	coagulation factor XIII, A1 polypeptide	coagulation factor XIII, A1 polypeptide
M26708_s_at	M26708_s_at	M26708	PASS	9	183.67	PASS	13	9	130.00	1.41	1.41	PTMA		prothymosin alpha	prothymosin alpha
K02777_s_at	K02777_s_at	K02777	PASS	7	25.86	PASS	13	7	18.31	1.41	1.41	TCRA	14q11.2	T-cell receptor, alpha (V.D.J.C)	T-cell receptor, alpha (V.D.J.C)
ITRAF	U59863_at	U59863	PASS	6	6.67	PASS	11	6	4.73	1.41	1.41	ITRAF		I-T-TRAF	I-T-TRAF
RPS24L	X62691_at	X62691	PASS	9	325.00	PASS	13	9	230.46	1.41	1.41	RPS15A	16p	ribosomal protein S15a	ribosomal protein S15a
MIH8	U37547_at	U37547	PASS	7	9.71	PASS	9	7	6.89	1.41	1.41	AP12	11q22	apoptosis inhibitor 2	apoptosis inhibitor 2
TRA2B	U68063_at	U68063	PASS	8	13.13	PASS	13	8	9.31	1.41	1.41	SPRS10	3q	splicing factor, arginine/serine-rich (transformer 2 Drosophila homolog) 10	splicing factor, arginine/serine-rich (transformer 2 Drosophila homolog) 10
POLR2F	Z27113_at	Z27113	PASS	9	22.33	PASS	13	9	15.85	1.41	1.41			RNA Polymerase II subunit	RNA Polymerase II subunit
RPL8	Z28407_at	Z28407	PASS	9	324.56	PASS	13	9	230.46	1.41	1.41	RPL8	8	ribosomal protein L8	ribosomal protein L8
K158_DIFF6	D63878_at	D63878	PASS	8	34.13	PASS	12	8	24.25	1.41	1.41	DIFF6	2q37	differentiation 6 (deoxyguanosine triphosphate triphosphohydrolase)	differentiation 6 (deoxyguanosine triphosphate triphosphohydrolase)
M97935_s_at	M97935_s_at	M97935	PASS	9	20.44	PASS	13	9	14.54	1.41	1.41			transcription factor (SGF-3)	transcription factor (SGF-3)
SI71	L40393_at	L40393	PASS	8	8.25	PASS	8	8	5.88	1.40	1.40	NUMB	14q24.3	numb (Drosophila) homolog	numb (Drosophila) homolog
HG3638-HT3	HG3638-HT3	HG3638-H	PASS	5	9.20	PASS	9	5	6.56	1.40	1.40				
K171_HYPL	D79993_at	D79993	PASS	6	7.83	PASS	12	6	5.58	1.40	1.40	KIAA0171		KIAA0171 gene product	KIAA0171 gene product
YSEC7	M85169_at	M85169	PASS	9	22.56	PASS	13	9	16.08	1.40	1.40	PSCD1	17q25	pleckstrin homology, Sec7 and coiled/coiled domains 1 (cytohesin 1)	pleckstrin homology, Sec7 and coiled/coiled domains 1 (cytohesin 1)
PRCP	L13977_at	L13977	PASS	9	14.67	PASS	11	9	10.45	1.40	1.40	PRCP	11q14	prolycarboxypeptidase (angiotensinase C)	prolycarboxypeptidase (angiotensinase C)

# Table 3: Feature 201

M4P	L03532 at AF006084	PASS	9	25.89	PASS	13	9	18.46	1.40	1.40	1.40	ARC41	M4 protein p41-Arc	WD repeat containing protein; similar to Sop216; 41 kD subunit of the Arp2/3 protein complex
K159	CHR1 D63880 at	PASS	8	7.00	PASS	9	8	5.00	1.40	1.40	1.40	KIAA0159		KIAA0159 gene product
E POV2	U18919 at	PASS	5	6.80	PASS	7	5	4.86	1.40	1.40	1.40	AQP3	aquaporin 3	aquaporin 3
AQP3	AB001325 at	PASS	9	20.56	PASS	13	9	14.69	1.40	1.40	1.40	P3	mitochondrial ATP synthase	
ATP5G3	U09813 at	PASS	9	33.44	PASS	13	9	23.92	1.40	1.40	1.40	STAT3	subunit 9 precursor	
STAT3	L29277 at	PASS	8	10.13	PASS	12	8	7.25	1.40	1.40	1.40	CSE1L	signal transducer and activator of transcription 3 (acute-phase response factor)	signal transducer and activator of transcription 3 (acute-phase response factor)
CSE1	U33286 at	PASS	8	8.75	PASS	11	8	6.27	1.39	1.39	1.39	HNRPG	chromosome segregation 1 (yeast homolog)-like	chromosome segregation 1 (yeast homolog)-like
HNRPG	Z23064 at	PASS	9	12.33	PASS	13	9	8.85	1.39	1.39	1.39	UBLI1	heterogeneous nuclear ribonucleoprotein G	heterogeneous nuclear ribonucleoprotein G
U61397 s at	U61397 s at	PASS	9	9.22	PASS	13	9	6.62	1.39	1.39	1.39	CD53	ubiquitin-like 1 (sentrin)	ubiquitin-like 1 (sentrin)
CD53	M37033 at	PASS	9	103.22	PASS	13	9	74.08	1.39	1.39	1.39	RPL7A	CD53 glycoprotein	CD53 antigen
RPL7A	M36072 at	PASS	9	272.56	PASS	13	9	195.62	1.39	1.39	1.39	MKNK1	ribosomal protein L7a	ribosomal protein L7a
ATP7A	AB000409 at	PASS	9	9.89	PASS	10	9	7.10	1.39	1.39	1.39	EIF3S8	MAP kinase-interacting serine/threonine kinase 1	MAP kinase-interacting serine/threonine kinase 1
RPS8	mal X67247 at	PASS	9	359.78	PASS	13	9	258.46	1.39	1.39	1.39	RPL6	ribosomal protein S8	ribosomal protein S8
K184	D80006 at	PASS	9	20.44	PASS	13	9	14.69	1.39	1.39	1.39	p62	ribosomal protein L6	ribosomal protein L6
RPL6	X69391 at	PASS	9	178.33	PASS	13	9	128.23	1.39	1.39	1.39	EIF3S8	ribosomal protein L6	ribosomal protein L6
SHGC	M88108 at	PASS	9	22.44	PASS	13	9	16.15	1.39	1.39	1.39	factor 3, subunit 8 (110kD)	ribosomal protein L6	ribosomal protein L6
K107	D14663 at	PASS	7	11.86	PASS	13	7	8.54	1.39	1.39	1.39	factor 3, subunit 8 (110kD)	ribosomal protein L6	ribosomal protein L6
EIF3	U46025 at	PASS	9	38.33	PASS	13	9	27.62	1.39	1.39	1.39	factor 3, subunit 8 (110kD)	ribosomal protein L6	ribosomal protein L6
K64	D31764 at	PASS	5	14.20	PASS	13	5	10.23	1.39	1.39	1.39	factor 3, subunit 8 (110kD)	ribosomal protein L6	ribosomal protein L6
PTPN12	M93425 at	PASS	9	16.22	PASS	13	9	11.69	1.39	1.39	1.39	factor 3, subunit 8 (110kD)	ribosomal protein L6	ribosomal protein L6
ACERA	U70063 at	PASS	7	13.71	PASS	9	7	9.89	1.39	1.39	1.39	factor 3, subunit 8 (110kD)	ribosomal protein L6	ribosomal protein L6
RPL5	HG4319-HT4	PASS	9	351.78	PASS	13	9	253.69	1.39	1.39	1.39	factor 3, subunit 8 (110kD)	ribosomal protein L6	ribosomal protein L6
ATPBPCD	D64158 at	PASS	7	8.57	PASS	11	7	6.18	1.39	1.39	1.39	factor 3, subunit 8 (110kD)	ribosomal protein L6	ribosomal protein L6
S100A10	M38591 at	PASS	9	75.56	PASS	13	9	54.54	1.39	1.39	1.39	factor 3, subunit 8 (110kD)	ribosomal protein L6	ribosomal protein L6
GP25L2	X90872 at	PASS	8	15.13	PASS	13	8	10.92	1.38	1.38	1.38	factor 3, subunit 8 (110kD)	ribosomal protein L6	ribosomal protein L6
K225_COSK	D86978 at	PASS	8	8.00	PASS	9	8	5.78	1.38	1.38	1.38	factor 3, subunit 8 (110kD)	ribosomal protein L6	ribosomal protein L6
SLC20A1	L20859 at	PASS	9	7.89	PASS	10	9	5.70	1.38	1.38	1.38	factor 3, subunit 8 (110kD)	ribosomal protein L6	ribosomal protein L6
U79528 s at	U79528 s at	PASS	9	15.00	PASS	13	9	10.85	1.38	1.38	1.38	factor 3, subunit 8 (110kD)	ribosomal protein L6	ribosomal protein L6
RPS5	U14970 at	PASS	9	293.11	PASS	13	9	212.00	1.38	1.38	1.38	factor 3, subunit 8 (110kD)	ribosomal protein L6	ribosomal protein L6
AFEX-HSAC	AFEX-HSAC	PASS	7	19.14	PASS	13	7	13.85	1.38	1.38	1.38	factor 3, subunit 8 (110kD)	ribosomal protein L6	ribosomal protein L6
MCM7	D55716 at	PASS	6	9.50	PASS	8	6	6.88	1.38	1.38	1.38	factor 3, subunit 8 (110kD)	ribosomal protein L6	ribosomal protein L6
PBP1	U83463 at	PASS	8	10.63	PASS	13	8	7.69	1.38	1.38	1.38	factor 3, subunit 8 (110kD)	ribosomal protein L6	ribosomal protein L6

# Top 25 in the cohort

MDCR	U72342_at	U72342	PASS	9	12.11	PASS	13	9	8.77	1.38	1.38	1.38	PFAH1B1	17p13.3-p13.3	platelet-activating factor acetylhydrolase, isoform 1b, alpha subunit (45kD)	platelet-activating factor acetylhydrolase, isoform 1b, alpha subunit (45kD)
RPI	L35035_at	L35035	PASS	8	7.25	PASS	8	8	5.25	1.38	1.38	1.38	UBE2D3		ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5)	ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5)
DDX	U90426_at	U90426	PASS	9	11.67	PASS	13	9	8.46	1.38	1.38	1.38			DEAD-box family member; contains DEAD-box; similar to rat liver nuclear protein p47 (PIR Accession Number A42881) and D. melanogaster DEAD-box RNA helicase WM6 (PIR Accession Number S51601)	DEAD-box family member; contains DEAD-box; similar to rat liver nuclear protein p47 (PIR Accession Number A42881) and D. melanogaster DEAD-box RNA helicase WM6 (PIR Accession Number S51601)
RPS25	M64716_at	M64716	PASS	9	275.67	PASS	13	9	200.15	1.38	1.38	1.38	RPS25	11q23.3	ribosomal protein S25	ribosomal protein S25
PSMB8_ma	Z14982_ma	Z14982	PASS	8	30.75	PASS	12	8	22.33	1.38	1.38	1.38	MHC- encoded proteasome subunit		alternative splicing	alternative splicing
HG3730-HT4	HG3730-HT4	HG3730-HT4	PASS	8	9.75	PASS	12	8	7.08	1.38	1.38	1.38				
RPL21	U25789_at	U25789	PASS	9	133.78	PASS	13	9	111.77	1.38	1.38	1.38	RPL21	13	ribosomal protein L21	ribosomal protein L21
DUT	U31930_at	U31930	PASS	9	11.11	PASS	13	9	8.08	1.38	1.38	1.38	DUT	15q15-q21.1	dUTP pyrophosphatase	dUTP pyrophosphatase
EIF4G2	D86549_at	D86549	PASS	8	6.88	PASS	11	8	5.00	1.38	1.38	1.38			p97 homologous protein	p97 homologous protein
K232	D86985_at	D86985	PASS	6	7.00	PASS	11	6	5.09	1.38	1.38	1.38	KIAA0232		KIAA0232 gene product	KIAA0232 gene product
PGD	U30255_at	U30255	PASS	6	22.00	PASS	10	6	16.00	1.38	1.38	1.38	PGD	1p36.3-p36.13	phosphogluconate dehydrogenase	phosphogluconate dehydrogenase
EMAPII	U10117_at	U10117	PASS	9	10.11	PASS	11	9	7.36	1.37	1.37	1.37	EMAPII		endothelial-monocyte activating polypeptide II	endothelial-monocyte activating polypeptide II
DSSI	U41515_at	U41515	PASS	9	8.78	PASS	10	9	6.40	1.37	1.37	1.37	DSSI		Method: conceptual translation supplied by author.	Method: conceptual translation supplied by author.
M14199_s_a	M14199_s_a	M14199	PASS	9	302.00	PASS	13	9	220.23	1.37	1.37	1.37	LAMR1	3p21.3	laminin receptor 1 (67kD); Ribosomal protein SA	laminin receptor 1 (67kD); Ribosomal protein SA
STXBP3	D63506_at	D63506	PASS	9	10.33	PASS	13	9	7.54	1.37	1.37	1.37	Munc-18.3		unc-18homologue	unc-18homologue
NME1	X17620_at	X17620	PASS	8	8.38	PASS	9	8	6.11	1.37	1.37	1.37	NME1	17q22	non-metastatic cells 1, protein (NM23A) expressed in	non-metastatic cells 1, protein (NM23A) expressed in
RPL3	X73460_at	X73460	PASS	9	364.22	PASS	13	9	265.77	1.37	1.37	1.37	RPL3	22	ribosomal protein L3	ribosomal protein L3
APEX	D13370_at	D13370	PASS	9	20.44	PASS	13	9	14.92	1.37	1.37	1.37	APEX	14q11.2-q12	APEX nuclease (multifunctional DNA repair enzyme)	APEX nuclease (multifunctional DNA repair enzyme)
K201	HSP10	D86956_at	PASS	6	7.00	PASS	9	6	5.11	1.37	1.37	1.37	KIAA0201		KIAA0201 gene product	KIAA0201 gene product
COX10_ma	U82010_ma	U82010	PASS	9	8.56	PASS	12	9	6.25	1.37	1.37	1.37	COX10	17p12-p11.2	cytochrome c oxidase subunit X (heme A: farnesyltransferase)	cytochrome c oxidase subunit X (heme A: farnesyltransferase)
LYZ_f	M19045_f_a	M19045	PASS	9	155.67	PASS	13	9	113.77	1.37	1.37	1.37	LYZ		lysosome precursor (EC 3.2.1.17)	lysosome precursor (EC 3.2.1.17)
RPL19	X63527_at	X63527	PASS	9	379.44	PASS	13	9	277.54	1.37	1.37	1.37	RPL19	17p12-q11	ribosomal protein L19	ribosomal protein L19
DPYD	U20938_at	U20938	PASS	8	9.25	PASS	13	8	6.77	1.37	1.37	1.37			dihydropyrimidine dehydrogenase	DPD; dihydropyrimidine dehydrogenase
Z47055_s_at	Z47055_s_at	Z47055	PASS	9	9.22	PASS	12	9	6.75	1.37	1.37	1.37	FDPS		farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, dimethylallyltransferase, geranyltransferase)	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, dimethylallyltransferase, geranyltransferase)



LYN	M16038_at	M16038	PASS	9	17.11	PASS	13	9	12.54	1.36	1.36	LYN	8q13	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
hum alu at	hum alu at	hum	PASS	9	422.44	PASS	13	9	309.62	1.36	1.36				
PCM1	L27841_at	L27841	PASS	6	7.83	PASS	8	6	5.75	1.36	1.36	PCM-1		pericentriolar material 1	
ACAA	D16294_at	D16294	PASS	8	9.13	PASS	10	8	6.70	1.36	1.36			mitochondrial 3-oxoacyl-CoA thiolase	
PSMA3	D00760_at	D00760	PASS	8	11.00	PASS	12	8	8.08	1.36	1.36	PSMA2	6q27	proteasome (prosome, macropain) subunit, alpha type, 2	proteasome (prosome, macropain) subunit, alpha type, 2
U07806_s_at	U07806_s_at	U07806	PASS	8	11.25	PASS	11	8	8.27	1.36	1.36			DNA topoisomerase 1	found in the camptothecin resistant clone CEM/C2
AB2KD	U15552_at	U15552	PASS	7	8.71	PASS	12	7	6.42	1.36	1.36			acidic 82 kDa protein	
D26535_s_at	D26535_s_at	D26535	PASS	8	10.00	PASS	11	8	7.36	1.36	1.36	DLST	14q24.3	dihydrofolate S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	dihydrofolate S-succinyltransferase (E2 component of 2-oxo-glutarate complex)
Z69148_s_at	Z69148_s_at	Z69148	PASS	9	285.33	PASS	13	9	210.23	1.36	1.36	RPL29	3q29-qter	ribosomal protein L29	ribosomal protein L29
EED	U90651_at	U90651	PASS	7	8.14	PASS	11	7	6.00	1.36	1.36	EED	11q14.2-q22.3	embryonic ectoderm development protein	embryonic ectoderm development protein
DYRK2	Y09216_at	Y09216	PASS	6	10.17	PASS	12	6	7.50	1.36	1.36	DYRK2	12	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2
LLREP3	X17206_at	X17206	PASS	9	471.00	PASS	13	9	347.46	1.36	1.36	RPS2	16p13.3	ribosomal protein S2	ribosomal protein S2
UBA52_maf	X56997_maf	X56997	PASS	9	268.44	PASS	13	9	198.08	1.36	1.36	UBA52		ubiquitin-52 amino acid fusion protein	
RPS18	X09150_at	X09150	PASS	9	377.78	PASS	13	9	278.77	1.36	1.36	RPS18	6p21.3	ribosomal protein S18	ribosomal protein S18
FCER2	M15059_at	M15059	PASS	9	9.33	PASS	9	9	6.89	1.35	1.35	FCER2	19p13.3	Fc fragment of IgE, low affinity II, receptor for (CD23A)	Fc fragment of IgE, low affinity II, receptor for (CD23A)
P87	L42572_at	L42572	PASS	8	8.38	PASS	11	8	6.18	1.35	1.35	p87/89		transmembrane protein	transmembrane protein
BTX_maf	U78027_maf	U78027	PASS	7	10.71	PASS	12	7	7.92	1.35	1.35	FTP3		lysosomal exoglycosidase	lysosomal exoglycosidase
HCG8	X92110_at	X92110	PASS	5	5.80	PASS	7	5	4.29	1.35	1.35				
PSKH1	U09564_at	U09564	PASS	8	7.50	PASS	11	8	5.55	1.35	1.35	SRPK1	6p21.2-p21.3	SFRS protein kinase 1	SFRS protein kinase 1
U09820_s_at	U09820_s_at	U09820	PASS	7	8.71	PASS	9	7	6.44	1.35	1.35	ATRX	Xq13.1-q21.1	helicase II	alpha thalassemia/mental retardation syndrome X-linked
U37546_s_at	U37546_s_at	U37546	PASS	8	7.13	PASS	11	8	5.27	1.35	1.35	AP11	11q22	apoptosis inhibitor 1	apoptosis inhibitor 1
S54005_s_at	S54005_s_at	S54005	PASS	9	184.44	PASS	13	9	136.54	1.35	1.35	thymosin beta-10		thymosin beta-10	This sequence comes from Fig. 1.
LKYHYD	U57721_at	U57721	PASS	9	9.44	PASS	13	9	7.00	1.35	1.35	KYNU		kynureninase; l-kynurenine hydrolase	kynureninase; l-kynurenine hydrolase
X95325_s_at	X95325_s_at	X95325	PASS	5	21.80	PASS	12	5	16.17	1.35	1.35	dbpAv		DNA-binding protein	variant A
RARS	S80343_at	S80343	PASS	8	7.50	PASS	7	8	5.57	1.35	1.35	RARS	5pter-q11	arginyl-tRNA synthetase	arginyl-tRNA synthetase
K148	D63482_at	D63482	PASS	5	7.80	PASS	10	5	5.80	1.34	1.34	KIAA0148		KIAA0148 gene product	KIAA0148 gene product
K178_SMC1	D80000_at	D80000	PASS	6	6.17	PASS	10	6	4.60	1.34	1.34	KIAA0178		similar to mitosis-specific chromosome segregation protein SMC1 of Saccharomyces	similar to mitosis-specific chromosome segregation protein SMC1 of Saccharomyces
RPS11	X06617_at	X06617	PASS	9	380.22	PASS	13	9	284.08	1.34	1.34	RPS11	19q13.3	ribosomal protein S11	ribosomal protein S11
JUN	U65928_at	U65928	PASS	8	8.75	PASS	11	8	6.55	1.34	1.34	JUN	1p32-p31	Avian sarcoma virus 17 (v-jun) oncogene homolog	v-jun avian sarcoma virus 17 oncogene homolog
INT6	U62962_at	U62962	PASS	9	52.67	PASS	13	9	39.46	1.33	1.33	EIF356	8q22-q23	murine mammary tumor integration site 6 (oncogene homolog)	murine mammary tumor integration site 6 (oncogene homolog)
RSU1	L12535_at	L12535	PASS	9	13.44	PASS	13	9	10.08	1.33	1.33	RSU-1		homologous to mouse Rsu-1; putative	homologous to mouse Rsu-1; putative

# Top 100 in The Enzyme

SFRS7_ma1	L41887_ma1	L41887	PASS	6	6.33	PASS	8	6	4.75	1.33	1.33	SFRS7	splicing factor, arginine/serine-rich 7	35 kDa protein
K71	D31888_at	D31888	PASS	8	7.25	PASS	9	8	5.44	1.33	1.33	KIAA0071		
ANT3	J01592_at	J01592	PASS	9	200.78	PASS	13	9	151.00	1.33	1.33	ANT3		adenine nucleotide translocator 3 (liver)
MDH1	D55654_at	D55654	PASS	9	25.56	PASS	13	9	19.23	1.33	1.33	KPNA4		cytosolic malate dehydrogenase
RPLP2	AB002533_s_at	AB002533	PASS	9	355.11	PASS	13	9	267.23	1.33	1.33	KPNA4		karyopherin alpha 4 (importin alpha 3)
PSMA5	D00761_at	D00761	PASS	9	33.11	PASS	13	9	24.92	1.33	1.33	PSMB1	7p13-p12	proteasome (prosome, macropain) subunit, beta type, 1
NPM1	M23613_at	M23613	PASS	9	103.33	PASS	13	9	77.85	1.33	1.33	NPM1	5q35	nucleophosmin
K2_TRIC5	D13627_at	D13627	PASS	9	15.78	PASS	12	9	11.92	1.32	1.32	KIAA0002		nucleophosmin (nucleolar phosphoprotein B23, numatrin)
GZMK	U26174_at	U26174	PASS	6	17.50	PASS	13	6	13.23	1.32	1.32	GZMK		KIAA0002 gene product
MRP	X78138_at	X78138	PASS	7	7.43	PASS	8	7	5.63	1.32	1.32	CD2	1p13	granzyme K (serine protease, granzyme 3; tryptase II)
M16316_s_at	M16316_s_at	M16316	PASS	9	52.11	PASS	13	9	39.54	1.32	1.32	CD2		CD2 antigen (p50), sheep red blood cell receptor
K164_DNAH	D79986_at	D79986	PASS	8	16.63	PASS	13	8	12.62	1.32	1.32	KIAA0164		KIAA0164 gene product
RPL17	X53777_at	X53777	PASS	9	206.44	PASS	13	9	156.69	1.32	1.32	RPL17	18q	ribosomal protein L17
SPHAR_ma1	X82554_ma1	X82554	PASS	5	6.00	PASS	9	5	4.56	1.32	1.32	SPHAR		ribosomal protein L17
SRC1	U59302_at	U59302	PASS	9	11.44	PASS	13	9	8.69	1.32	1.32	SRC1	2p23	steroid receptor coactivator 1
FLI1	M98833_at	M98833	PASS	7	8.29	PASS	13	7	6.31	1.31	1.31	FLI1	11q24.1-q24.3	Friend leukemia virus integration 1
K16	D13641_at	D13641	PASS	8	13.13	PASS	13	8	10.00	1.31	1.31	KIAA0016		Friend leukemia virus integration 1
TFAP3S	U91932_at	U91932	PASS	9	14.33	PASS	13	9	10.92	1.31	1.31	CLAP3	12p13.2-p13.1	mitochondrial outer membrane protein 19
GUA5MPST	HG4716-HT	HG4716-H	PASS	8	7.75	PASS	11	8	5.91	1.31	1.31	CLAP3		clathrin-associated/assembly/adaptor protein, small 3, 22-kD; Signa3A
RPS28	U58682_at	U58682	PASS	9	286.67	PASS	13	9	218.69	1.31	1.31	RPS28	19p13.2	ribosomal protein S28
RAB11A	AF000231_at	AF000231	PASS	6	6.17	PASS	7	6	4.71	1.31	1.31	RPS28		ribosomal protein S28
AFEX-HUM4	AFEX-HUM4	AFEX-HUN	PASS	6	12.17	PASS	13	6	9.31	1.31	1.31	RAB11A		GTPase
HPRT1	M31642_at	M31642	PASS	8	7.63	PASS	12	8	5.83	1.31	1.31	HPRT1	Xq26.1	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)
PSM112	D44466_at	D44466	PASS	9	7.44	PASS	10	9	5.70	1.31	1.31	PSMD1		hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)
PEBP2AC1	Z35278_at	Z35278	PASS	9	19.78	PASS	13	9	15.15	1.31	1.31	CBFA3	1p36	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1
PSMCP31	D38047_at	D38047	PASS	9	31.22	PASS	13	9	23.92	1.31	1.31	PSMD8		core-binding factor, runt domain, alpha subunit 3
PSM42	D78275_at	D78275	PASS	8	9.25	PASS	10	8	7.10	1.30	1.30	PSMC6	12q15	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8
P76	U81006_at	U81006	PASS	7	9.00	PASS	11	7	6.91	1.30	1.30	P76		proteasome (prosome, macropain) 26S subunit, ATPase, 6
K54_MOV10	D29677_at	D29677	PASS	7	8.29	PASS	11	7	6.36	1.30	1.30	KIAA0054		76 kDa membrane protein
SKIP	U51432_at	U51432	PASS	6	13.00	PASS	10	6	10.00	1.30	1.30	SKIP		KIAA0054 gene product

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K256	D87445_at	D87445	PASS	6	6.50	PASS	9	6	5.00	1.30	1.30	KIAA0256			KIAA0256 gene product
LGALS8	L78132_at	L78132	PASS	6	6.17	PASS	8	6	4.75	1.30	1.30	pea-1			prostate carcinoma tumor antigen
POLR2	U37689_at	U37689	PASS	5	9.80	PASS	9	5	7.56	1.30	1.30	hsRPB8	2q33-q34		RNA polymerase II subunit
CASP10	U60519_at	U60519	PASS	6	6.67	PASS	7	6	5.14	1.30	1.30	CASP10	4q21-q24		caspase 10, apoptosis-related cysteine protease
L14778_s_at	L14778_s_at	L14778	PASS	9	9.78	PASS	11	9	7.55	1.30	1.30	PPP3CA	4q21-q24		protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha)
RAB_mal1	L42025_mal1	L42025	PASS	6	6.33	PASS	9	6	4.89	1.30	1.30	HRB	2q36		HIV-1 Rev binding protein
GAPDH	AFEX-HUMC	AFEX-HUMC	PASS	9	162.00	PASS	13	9	125.31	1.29	1.29				HIV-1 Rev binding protein
E_121711DM	U92014_at	U92014	PASS	6	6.83	PASS	7	6	5.29	1.29	1.29				
HRMT1L1	X99209_at	X99209	PASS	9	20.78	PASS	13	9	16.08	1.29	1.29				arginine methyltransferase
RPL10	HG4542-HT4	HG4542-HT4	PASS	9	184.78	PASS	13	9	143.08	1.29	1.29				
28SRNA5	AFEX-M278	AFEX-M278	PASS	7	8.71	PASS	8	7	6.75	1.29	1.29				
YWHA	X56468_at	X56468	PASS	9	23.33	PASS	13	9	18.08	1.29	1.29				14.3.3 protein
ACADM	M91432_at	M91432	PASS	8	7.50	PASS	11	8	5.82	1.29	1.29	ACADM	1p31		acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain
FMRI	U25165_at	U25165	PASS	7	11.00	PASS	13	7	8.54	1.29	1.29	FXR1	3q28		fragile X mental retardation, autosomal homolog 1
HMG17_mal1	X13546_mal1	X13546	PASS	9	40.22	PASS	13	9	31.23	1.29	1.29	HMG17	1p36.1-p35		high-mobility group (nonhistone chromosomal) protein 17
K6_VAV1	D25304_at	D25304	PASS	9	16.11	PASS	13	9	12.54	1.28	1.28	KIAA0006			PAK-interacting exchange factor
SNRPD2	U15008_at	U15008	PASS	9	140.33	PASS	13	9	109.23	1.28	1.28	SNRPD2			small nuclear ribonucleoprotein D2 polypeptide (16.5kD)
COX5A	M22760_at	M22760	PASS	9	16.89	PASS	13	9	13.15	1.28	1.28	COX5A	15q25		cytochrome c oxidase subunit Va
VRK1	AB000449	AB000449	PASS	7	7.57	PASS	10	7	5.90	1.28	1.28	VRK1	14q32		vaccinia related kinase 1
M31516_s_a	M31516_s_a	M31516	PASS	5	6.20	PASS	12	5	4.83	1.28	1.28	DAF	1q32		decay accelerating factor for complement (CD55, Cromer blood group system)
TRPSL	M23161_at	M23161	PASS	7	6.29	PASS	11	7	4.91	1.28	1.28				proteasome (prosome, macropain) 26S subunit, ATPase, 5
PSMC5	L38810_at	L38810	PASS	9	14.67	PASS	11	9	11.45	1.28	1.28	PSMC5	17q23-q25		proteasome (prosome, macropain) 26S subunit, ATPase, 5
UROD	M14016_at	M14016	PASS	7	7.86	PASS	7	7	6.14	1.28	1.28	UROD	1p34		uroporphyrinogen decarboxylase
POLR2	HG2274-HT2	HG2274-HT2	PASS	6	10.33	PASS	12	6	8.08	1.28	1.28				uroporphyrinogen decarboxylase
M96954_s_a	M96954_s_a	M96954	PASS	9	7.67	PASS	13	9	6.00	1.28	1.28				nucleolysin TIAR
TRP185	U38847_at	U38847	PASS	5	6.20	PASS	7	5	4.86	1.28	1.28	TRP-185			TAR RNA loop binding protein
GCNT1	U77413_at	U77413	PASS	5	7.40	PASS	10	5	5.80	1.28	1.28	OGT			O-linked N-acetylglucosamine (GlcNAc) transferase (uridine diphospho-N-acetylglucosamine:polypeptide-beta-N-acetylglucosaminyl transferase)
RAN	HG1112-HT	HG1112-HT	PASS	9	21.44	PASS	13	9	16.85	1.27	1.27				inducible poly(A)-binding protein
INDPOLAB1	U33818_at	U33818	PASS	8	14.88	PASS	13	8	11.69	1.27	1.27	IPABP			dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit
DPM1	AF007875_at	AF007875	PASS	8	8.38	PASS	12	8	6.58	1.27	1.27	DPM1			dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit

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TCF3	M31523_at	M31523	PASS	9	6.89	PASS	12	9	5.42	1.27	1.27	1.27	TCF3	19	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)
Z26491_s_at	Z26491_s_at	Z26491	PASS	9	13.89	PASS	13	9	10.92	1.27	1.27	1.27	HNRPD	4q21	catechol O-methyltransferase
HNRNPCL	M94630_at	M94630	PASS	9	27.36	PASS	13	9	21.69	1.27	1.27	1.27	HNRPD	4q21	heterogeneous nuclear ribonucleoprotein D
K212_COSC	D86967_at	D86967	PASS	7	11.43	PASS	12	7	9.00	1.27	1.27	1.27	KIAA0212		KIAA0212 gene product
EIF2A	U26032_at	U26032	PASS	5	5.80	PASS	7	5	4.57	1.27	1.27	1.27	TCFBR2	3p22	transforming growth factor, beta receptor II (70-80kD)
TCFBR2	D50683_at	D50683	PASS	9	24.00	PASS	13	9	18.92	1.27	1.27	1.27	TCFBR2	3p22	transforming growth factor, beta receptor II (70-80kD)
PPP2R2A	M64929_at	M64929	PASS	7	7.29	PASS	8	7	5.75	1.27	1.27	1.27	PPP2R2A		protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform
GPRK5	L15388_at	L15388	PASS	6	6.33	PASS	7	6	5.00	1.27	1.27	1.27	GPRK5	10q24-qter	G protein-coupled receptor kinase 5
PPP3CB2	M29551_at	M29551	PASS	5	7.60	PASS	9	5	6.00	1.27	1.27	1.27			calcineurin A2
HG3484-HT2	HG3484-HT2	HG3484-HT2	PASS	7	8.86	PASS	12	7	7.00	1.27	1.27	1.27			cyclin H
CCNH	U11791_at	U11791	PASS	7	6.43	PASS	12	7	5.08	1.26	1.26	1.26	CCNH	5q13.3-q14	H2A histone family, member Q
H2B_ma2	X57985_ma2	X57985	PASS	9	9.11	PASS	13	9	7.23	1.26	1.26	1.26	H2AFQ	1q21-q23	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)
NFKB1	M38603_at	M38603	PASS	6	16.17	PASS	12	6	12.83	1.26	1.26	1.26	NFKB1	4q24	thyroid autoantigen 70kD (Ku antigen)
G22P1	J04611_at	J04611	PASS	9	23.44	PASS	13	9	18.62	1.26	1.26	1.26	G22P1	22q11-q13	Rab geranylgeranyltransferase, beta subunit
RABGGTB	X98001_at	X98001	PASS	6	6.67	PASS	10	6	5.30	1.26	1.26	1.26	RABGGTB	1p31-p22	enoyl Coenzyme A hydratase 1, peroxisomal
ECH1	U16660_at	U16660	PASS	7	20.37	PASS	13	7	16.38	1.26	1.26	1.26	ECH1	19q13.1	Similar to S.cerevisiae hypothetical protein L3111 (S59316)
K276_HYPL	D87466_at	D87466	PASS	7	5.71	PASS	9	7	4.56	1.25	1.25	1.25	KIAA0276		RAD21 (S. pombe) homolog
K78_RAD21	D38551_at	D38551	PASS	8	10.63	PASS	12	8	8.50	1.25	1.25	1.25	RAD21		endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
ECGF1	M31210_at	M31210	PASS	8	6.38	PASS	10	8	5.10	1.25	1.25	1.25	EDG1	1pter-qter	catechol-O-methyltransferase
M58525_s_a	M58525_s_a	M58525	PASS	5	10.40	PASS	12	5	8.33	1.25	1.25	1.25	COMT	22q11.21-q11.23	zinc finger protein 43 (HTF6)
HG2639-HT2	HG2639-HT2	HG2639-HT2	PASS	9	11.89	PASS	13	9	9.54	1.25	1.25	1.25			zinc finger protein 43 (HTF6)
ZNF43_f	X39244_f_at	X39244	PASS	5	5.60	PASS	10	5	4.50	1.24	1.24	1.24	ZNF43	19p13.1-p12	macrophage migration inhibitory factor (glycosylation-inhibiting factor)
D79984_s_at	D79984_s_at	D79984	PASS	5	6.40	PASS	7	5	5.14	1.24	1.24	1.24	KIAA0162		interleukin 16 (lymphocyte chemoattractant factor)
MIF_ma1	L19686_ma1	L19686	PASS	9	43.33	PASS	13	9	34.85	1.24	1.24	1.24	MIF	22q11.2	cathepsin S
CBF	M37197_at	M37197	PASS	8	6.75	PASS	7	8	5.43	1.24	1.24	1.24	CEBP		enhancer of rudimentary (Drosophila) homolog
M90391_s_a	M90391_s_a	M90391	PASS	7	7.71	PASS	9	7	6.22	1.24	1.24	1.24	IL16		interleukin 16 (lymphocyte chemoattractant factor)
K29	D21852_at	D21852	PASS	9	7.33	PASS	12	9	5.92	1.24	1.24	1.24	KIAA0029		cathepsin S
CTSS	M90696_at	M90696	PASS	8	12.38	PASS	11	8	10.00	1.24	1.24	1.24	CTSS	1q21	enhancer of rudimentary (Drosophila) homolog
X15673_s_at	X15673_s_at	X15673	PASS	5	9.40	PASS	10	5	7.60	1.24	1.24	1.24			
ERH	D85758_at	D85758	PASS	7	21.86	PASS	13	7	17.69	1.24	1.24	1.24	ERH	7q34	



# Table 2001

HADHB	DI6481_at	DI6481	PASS	6	9.17	PASS	13	6	7.54	1.22	1.22	1.21	1.21	HADHB	2p23	hydroxycyl-Coenzyme A dehydrogenase/3-ketocyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	hydroxycyl-Coenzyme A dehydrogenase/3-ketocyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit
PCSK4	HG4297-HT4		PASS	9	24.00	PASS	13	9	19.77	1.21	1.21	1.21	1.21	ATM	11q22-q23	ataxia telangiectasia mutated (includes complementation groups A, C and D)	ataxia telangiectasia mutated (includes complementation groups A, C and D)
ATM	U33841_at	U33841	PASS	5	6.20	PASS	9	5	5.11	1.21	1.21	1.21	1.21				
RPL31	X15940_at	X15940	PASS	9	354.56	PASS	13	9	292.46	1.21	1.21	1.21	1.21	RPL31	2	ribosomal protein L31	ribosomal protein L31
BTX ma3	U78027_ma3	U78027	PASS	9	174.44	PASS	13	9	144.08	1.21	1.21	1.21	1.21	FTP3		lysosomal exoglycosidase	lysosomal exoglycosidase
X15729_s_at	X15729_s_at	X15729	PASS	9	36.56	PASS	13	9	30.23	1.21	1.21	1.21	1.21	DDX5	17q21	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase, 68kD)	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase, 68kD)
DNAPKCS	U47077_at	U47077	PASS	7	5.29	PASS	8	7	4.38	1.21	1.21	1.21	1.21	PRKDC	8q11	DNA-dependent protein kinase catalytic subunit	protein kinase, DNA-activated, catalytic polypeptide
CUL3	U58089_at	U58089	PASS	8	9.75	PASS	13	8	8.08	1.21	1.21	1.21	1.21	CUL3	Chr.2	cullin 3	cullin 3
D28473_s_at	D28473_s_at	D28473	PASS	6	6.33	PASS	12	6	5.25	1.21	1.21	1.21	1.21	IARS	9q21	isoleucine-tRNA synthetase	isoleucine-tRNA synthetase
J04029_s_at	J04029_s_at	J04029	PASS	9	9.56	PASS	13	9	7.92	1.21	1.21	1.21	1.21	KRT10	17q21-q23	keratin 10	keratin 10 (epidermolytic hyperkeratosis; keratolysis palmaris et plantaris)
CDC16HS	U18291_at	U18291	PASS	6	6.83	PASS	12	6	5.67	1.21	1.21	1.21	1.21	CDC16		cell division cycle 16; anaphase promoting complex 6	cell division cycle 16; anaphase promoting complex 6
HSPE1	U07550_at	U07550	PASS	7	7.43	PASS	11	7	6.18	1.20	1.20	1.20	1.20	HSPE1		heat shock 10kD protein 1 (chaperonin 10)	heat shock 10kD protein 1 (chaperonin 10)
BTX f	HG1515-HT	HG1515-H	PASS	9	63.44	PASS	13	9	52.85	1.20	1.20	1.20	1.20				
CD86	U04343_at	U04343	PASS	8	6.00	PASS	9	8	5.00	1.20	1.20	1.20	1.20	CD86		CD86 antigen	common synonyms are B7-2 and B70; B70 antigen; B7-2
K11	D13636_at	D13636	PASS	6	7.50	PASS	8	6	6.25	1.20	1.20	1.20	1.20	GTF3C2	2	general transcription factor IIIC, polypeptide 2 (beta subunit, 110kD)	general transcription factor IIIC, polypeptide 2 (beta subunit, 110kD)
SEMAE	AB000220_a	AB000220	PASS	5	6.00	PASS	8	5	5.00	1.20	1.20	1.20	1.20			senaphorin E	translocation protein 1
TRANSPI	D87127_at	D87127	PASS	5	6.60	PASS	8	5	5.50	1.20	1.20	1.20	1.20	TLOC1		translocation protein 1	translocation protein 1
X75755_ma	X75755_ma	X75755	PASS	7	6.43	PASS	11	7	5.36	1.20	1.20	1.20	1.20	SFRS2	17	splicing factor, arginine/serine-rich 2	splicing factor, arginine/serine-rich 2
PTPN4	M68941_at	M68941	PASS	7	7.86	PASS	9	7	6.56	1.20	1.20	1.20	1.20	PTPN4		protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte)	protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte)
TAF2G	U21858_at	U21858	PASS	8	7.00	PASS	13	8	5.85	1.20	1.20	1.20	1.20	TAF2G		TATA box binding protein (TBP)-associated factor, RNA polymerase II, G, 32kD	TATA box binding protein (TBP)-associated factor, RNA polymerase II, G, 32kD
PIGB	D42138_at	D42138	PASS	6	5.83	PASS	8	6	4.88	1.20	1.20	1.20	1.20	PIGB	15q21-q22	phosphatidylinositol glycan, class B	phosphatidylinositol glycan, class B
U50527_s_at	U50527_s_at	U50527	PASS	6	5.67	PASS	8	6	4.75	1.19	1.19	1.19	1.19				
PYGL	M14636_at	M14636	PASS	7	5.71	PASS	10	7	4.80	1.19	1.19	1.19	1.19	PYGL	14q11.2-q24.3	phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)	phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)
PSMZ	D38048_at	D38048	PASS	9	10.89	PASS	13	9	9.15	1.19	1.19	1.19	1.19	PSMB7	9q34.11-q34.12	proteasome (prosome, macropain) subunit, beta type, 7	proteasome (prosome, macropain) subunit, beta type, 7
CASP4	U28014_at	U28014	PASS	9	23.33	PASS	13	9	19.62	1.19	1.19	1.19	1.19	CASP4	11q22.2-q22.3	caspase 4, apoptosis-related cysteine protease	caspase 4, apoptosis-related cysteine protease



ERP31	X94910_at	X94910	PASS	8	19.25	PASS	13	8	16.46	1.17	1.17	ERp28	Similar to ULA_5 product, AC P30040
TCPI	X52882_at	X52882	PASS	8	11.38	PASS	12	8	9.75	1.17	1.17		i-complex polypeptide 1 (AA 1-556)
DAP5	AFFX-DnpX-AFFX-Dnp		PASS	9	242.44	PASS	13	9	207.85	1.17	1.17		
SGTBP	U57094_at	U57094	PASS	6	11.00	PASS	9	6	9.44	1.16	1.16	RAB27A, member RAS oncogene family	RAB27A, member RAS oncogene family
SF2P32	M69039_at	M69039	PASS	8	9.13	PASS	13	8	7.85	1.16	1.16	complement component 1, q subcomponent binding protein	complement component 1, q subcomponent binding protein
UBE2A	M74524_at	M74524	PASS	7	6.00	PASS	12	7	5.17	1.16	1.16	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	ubiquitin-conjugating enzyme E2A (RAD6 homolog)
CCT4	U38846_at	U38846	PASS	9	30.67	PASS	13	9	26.46	1.16	1.16	stimulator of TAR RNA binding	stimulator of TAR RNA binding
FRG1	L76159_at	L76159	PASS	6	7.67	PASS	13	6	6.62	1.16	1.16	FSHD region gene 1	FSHD region gene 1
M57466_s_at	M57466_s_at	M57466	PASS	9	70.67	PASS	13	9	61.08	1.16	1.16	major histocompatibility complex, class II, DP beta 1	major histocompatibility complex, class II, DP beta 1
U44799_s_at	U44799_s_at	U44799	PASS	6	6.00	PASS	10	6	5.20	1.15	1.15	U1-snRNP binding protein homolog	U1-snRNP binding protein homolog
RASA1	M23379_at	M23379	PASS	5	6.00	PASS	10	5	5.20	1.15	1.15	RAS p21 protein activator (GTPase activating protein) 1	RAS p21 protein activator (GTPase activating protein) 1
J02621_s_at	J02621_s_at	J02621	PASS	9	26.44	PASS	13	9	22.92	1.15	1.15	high-mobility group (nonhistone chromosomal) protein 14	high-mobility group (nonhistone chromosomal) protein 14
YES1	M15990_at	M15990	PASS	7	5.43	PASS	7	7	4.71	1.15	1.15	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1
CTSL	X12451_at	X12451	PASS	6	6.33	PASS	10	6	5.50	1.15	1.15	cathepsin L	cathepsin L
W19119	M24069_at	M24069	PASS	7	6.71	PASS	12	7	5.83	1.15	1.15	cold shock domain protein A	cold shock domain protein A
Z25521_s_at	Z25521_s_at	Z25521	PASS	9	16.11	PASS	13	9	14.00	1.15	1.15	integrin associated protein	integrin associated protein
CISACTS	M82882_at	M82882	PASS	7	7.86	PASS	12	7	6.83	1.15	1.15	E74-like factor 1 (ets domain transcription factor)	E74-like factor 1 (ets domain transcription factor)
K181	D80003_at	D80003	PASS	8	6.13	PASS	12	8	5.33	1.15	1.15		
CAMLG	U18242_at	U18242	PASS	7	6.57	PASS	11	7	5.73	1.15	1.15	calcium modulating ligand	calcium modulating ligand
RANBP1	D38076_at	D38076	PASS	7	9.00	PASS	13	7	7.85	1.15	1.15	RAN binding protein 1	RAN binding protein 1
ICT1	X81788_at	X81788	PASS	7	6.14	PASS	11	7	5.36	1.15	1.15	immature colon carcinoma transcript 1	immature colon carcinoma transcript 1
RB1	L41870_at	L41870	PASS	7	5.86	PASS	8	7	5.13	1.14	1.14	retinoblastoma 1 (including osteosarcoma)	retinoblastoma 1 (including osteosarcoma)
K254	D87443_at	D87443	PASS	7	4.57	PASS	7	7	4.00	1.14	1.14	KIAA0254 gene product	KIAA0254 gene product
HG1428-HT	HG1428-HT	HG1428-HT	PASS	9	286.67	PASS	13	9	230.92	1.14	1.14		
M31520_ma	M31520_ma	M31520	PASS	9	154.78	PASS	13	9	135.54	1.14	1.14	ribosomal protein S24	ribosomal protein S24
NAP1L1	M86667_at	M86667	PASS	9	33.78	PASS	13	9	29.62	1.14	1.14	nucleosome assembly protein 1-like 1	nucleosome assembly protein 1-like 1
RBM3	U28686_at	U28686	PASS	8	12.13	PASS	11	8	10.64	1.14	1.14	RNA binding motif protein 3	RNA binding motif protein 3
U58046_s_at	U58046_s_at	U58046	PASS	5	5.80	PASS	10	5	5.10	1.14	1.14	eukaryotic translation initiation factor 3, subunit 10 (theta, 170KD)	eukaryotic translation initiation factor 3, subunit 10 (theta, 170KD)
VBP1	U56833_at	U56833	PASS	8	6.38	PASS	13	8	5.62	1.14	1.14	von Hippel-Lindau binding protein 1	von Hippel-Lindau binding protein 1
TCLLYM_ma	X82240_ma	X82240	PASS	5	15.20	PASS	12	5	13.42	1.13	1.13	T-cell leukemia/lymphoma 1A	T-cell leukemia/lymphoma 1A
ACP1	U25849_at	U25849	PASS	6	9.83	PASS	13	6	8.69	1.13	1.13	acid phosphatase 1, soluble	acid phosphatase 1, soluble
M60483_ma	M60483_ma	M60483	PASS	8	6.50	PASS	12	8	5.75	1.13	1.13	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform



# FOURTH FLOOR

PSMHCB	D00762_at	D00762	PASS	7	11.43	PASS	9	7	10.11	1.13	1.13	PSMA3	14q23	proteasome (prosome, macropain) subunit, alpha type, 3	proteasome (prosome, macropain) subunit, alpha type, 3
LGALS2	M87860_at	M87860	PASS	7	26.71	PASS	11	7	23.64	1.13	1.13	LGALS2		S-lac lectin	
D11327_s_at	D11327_s_at	D11327	PASS	8	5.75	PASS	10	8	5.10	1.13	1.13	PTPN7	1q32.1	protein tyrosine phosphatase, non-receptor type 7	protein tyrosine phosphatase, non-receptor type 7
EPF3	L34587_at	L34587	PASS	9	13.78	PASS	13	9	12.23	1.13	1.13			RNA polymerase II elongation factor SIII, p15 subunit	putative
FEZ2	U60061_at	U60061	PASS	6	5.83	PASS	11	6	5.18	1.13	1.13	FEZ2		FEZ2	zygyn 2
U49020_cd5	U49020_cd5	U49020	PASS	8	5.75	PASS	9	8	5.11	1.13	1.13	MEF2A		myocyte-specific enhancer factor 2A, C4 form	
PPM1A	S87759_at	S87759	PASS	7	6.00	PASS	9	7	5.33	1.13	1.13	PPM1B		protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform	protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform
EIF4A2	D30655_at	D30655	PASS	9	60.56	PASS	13	9	53.85	1.12	1.12	EIF4A2	18p11.2	eukaryotic translation initiation factor 4A, isoform 2	eukaryotic translation initiation factor 4A, isoform 2
GRLB	HG4582-HT4	HG4582-HT	PASS	5	5.60	PASS	11	5	5.00	1.12	1.12	TPMT		thiopurine methyltransferase	35 kDa monomer; cytosolic protein
U12387_s_at	U12387_s_at	U12387	PASS	5	6.60	PASS	10	5	5.90	1.12	1.12				
AICL	X96719_at	X96719	PASS	5	18.40	PASS	13	5	16.46	1.12	1.12	CLECSF2	12p	C-Type lectin	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced)
K69_DS0556	D31885_at	D31885	PASS	9	16.56	PASS	13	9	14.85	1.12	1.12	KIAA0069			
PSMA5	X61970_at	X61970	PASS	9	13.11	PASS	13	9	11.77	1.11	1.11	PSMA5	1p13	proteasome (prosome, macropain) subunit, alpha type, 5	proteasome (prosome, macropain) subunit, alpha type, 5
PRPS1	D00860_at	D00860	PASS	9	6.11	PASS	12	9	5.50	1.11	1.11	PRPS1	Xq21-q27	phosphoribosyl pyrophosphate synthetase 1	phosphoribosyl pyrophosphate synthetase 1
U33936_s_at	U33936_s_at	U33936	PASS	7	5.86	PASS	11	7	5.27	1.11	1.11	ADK	10cen-q24	adenosine kinase	adenosine kinase
LCP2	U20158_at	U20158	PASS	9	17.00	PASS	13	9	15.31	1.11	1.11			SLP-76	76 kDa tyrosine phosphoprotein
HG2981-HT	HG2981-HT	HG2981-HT	PASS	7	10.29	PASS	11	7	9.27	1.11	1.11				
PP1B	M63573_at	M63573	PASS	7	17.29	PASS	12	7	15.58	1.11	1.11	PP1B	15	peptidylprolyl isomerase B (cyclophilin B)	peptidylprolyl isomerase B (cyclophilin B)
B56E	L76703_at	L76703	PASS	6	5.17	PASS	9	6	4.67	1.11	1.11	PPP2R5E	7p11.2-p12	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform
E_23801	U79282_at	U79282	PASS	5	5.20	PASS	10	5	4.70	1.11	1.11				
HSPA8	HG2855-HT	HG2855-HT	PASS	9	38.56	PASS	13	9	35.00	1.10	1.10				
H2AZ	M37583_at	M37583	PASS	9	18.11	PASS	13	9	16.46	1.10	1.10	H2AFZ	4q24	H2A histone family, member Z	H2A histone family, member Z
PHC11	J04973_at	J04973	PASS	9	12.78	PASS	13	9	11.62	1.10	1.10	UQCRC2	16p12	ubiquinol-cytochrome c reductase core protein II	ubiquinol-cytochrome c reductase core protein II
TCRD	M21624_at	M21624	PASS	9	17.33	PASS	13	9	15.77	1.10	1.10	TCRD	14q11.2	T-cell receptor, delta (V.D.J.C)	T-cell receptor, delta (V.D.J.C)
TNFAIP3	M59465_at	M59465	PASS	9	13.33	PASS	13	9	12.15	1.10	1.10	TNFAIP1	17q22-q23	A20	tumor necrosis factor, alpha-induced protein 1 (endothelial)
APBB1	U50939_at	U50939	PASS	7	6.57	PASS	12	7	6.00	1.10	1.10	APPBP1	16q22	Anyloid beta precursor protein-binding protein 1	Anyloid beta precursor protein-binding protein 1, 59kD
BACTINM	AFFX-HSAC	AFFX-HSAC	PASS	9	330.67	PASS	13	9	302.92	1.09	1.09				
D13824E	U47635_at	U47635	PASS	6	6.67	PASS	9	6	6.11	1.09	1.09				DSEB number: D13824E; orf
RAD23B	D21090_at	D21090	PASS	7	6.00	PASS	12	7	5.50	1.09	1.09	RAD23B	3p25.1	RAD23 (S. cerevisiae) homolog B	RAD23 (S. cerevisiae) homolog B

PSMD4	U24704_at	U24704	PASS	7	11.29	PASS	11	7	10.36	1.09	1.09	antiseretory factor-1	similar to Human S5a proteasome subunit, Genbank Accession Number U51007
PRKMK1	L11284_at	L11284	PASS	7	10.29	PASS	13	7	9.46	1.09	1.09	15q22.1-q22.33	protein kinase, mitogen-activated, kinase 1 (MAP kinase kinase 1)
BI0B5	AFFX-BioB-AFFX-BioB	L13848_at	PASS	9	113.56	PASS	13	9	104.69	1.08	1.08	1q25	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA helicase A, nuclear DNA helicase II; leukophycin)
LKP	L13848_at	L13848	PASS	6	10.83	PASS	10	6	10.00	1.08	1.08		
EFTS	L37936_at	L37936	PASS	8	10.38	PASS	12	8	9.58	1.08	1.08		elongation factor Ts
CBX	U35451_at	U35451	PASS	6	6.17	PASS	10	6	5.70	1.08	1.08		heterochromatin protein p25
SMN1_mn3	U80017_mn3	U80017	PASS	7	6.00	PASS	9	7	5.56	1.08	1.08		basic transcription factor 2 p44
X03689_s_at	X03689_s_at	X03689	PASS	9	224.56	PASS	13	9	208.08	1.08	1.08	20q13.3	eukaryotic translation elongation factor 1 alpha 2
PRPS2	Y00971_at	Y00971	PASS	5	5.00	PASS	11	5	4.64	1.08	1.08	Xpter-q21	phosphoribosyl pyrophosphate synthetase 2
ATP5C1	D16562_at	D16562	PASS	9	29.67	PASS	13	9	27.54	1.08	1.08		L(liver)-type ATP synthase gamma-subunit
K191	D83776_at	D83776	PASS	5	6.00	PASS	7	5	5.57	1.08	1.08	KIAA0191	The KIAA0191 gene is expressed ubiquitously; The KIAA0191 protein retains the C2H2 zinc-finger at its N-terminal region.
M67468_s_at	M67468_s_at	M67468	PASS	7	5.14	PASS	9	7	4.78	1.08	1.08	Xq27.3	fragile X mental retardation 1
ANX7	J04543_at	J04543	PASS	8	8.25	PASS	12	8	7.67	1.08	1.08	10q21.1-q21.12	annexin VII (synexin)
CMKBR7	L08177_at	L08177	PASS	8	5.38	PASS	10	8	5.00	1.08	1.08	EBI 2: EBV induced G-protein coupled receptor	Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor)
NIFUL	U47101_at	U47101	PASS	9	26.78	PASS	13	9	24.92	1.07	1.07	hNifU	Similar to N-terminal regions of diazotroph NifU proteins
K242_HYP5	D87684_at	D87684	PASS	8	8.13	PASS	10	8	7.60	1.07	1.07	KIAA0242	similar to a C.elegans ZK353.8 protein (S44655)
LCP1	J02923_at	J02923	PASS	9	45.67	PASS	13	9	42.77	1.07	1.07	13q14.3	lymphocyte cytosolic protein 1 (L-plasin)
SZ03_15	L40395_at	L40395	PASS	8	6.50	PASS	9	8	6.11	1.06	1.06		ORF; putative
LAML	HG1078-HT	HG1078-HT	PASS	7	13.00	PASS	13	7	12.23	1.06	1.06		pre-B-cell leukemia transcription factor 3
PBX3	X59841_at	X59841	PASS	6	5.67	PASS	9	6	5.33	1.06	1.06	9q33-q34	homeobox protein
SRP9	U20998_at	U20998	PASS	9	15.44	PASS	13	9	14.54	1.06	1.06		signal recognition particle 9kD
L33930_s_at	L33930_s_at	L33930	PASS	6	4.67	PASS	10	6	4.40	1.06	1.06		signal transducer CD24
CGR19	U66469_at	U66469	PASS	5	5.40	PASS	10	5	5.10	1.06	1.06		cell growth regulator CGR19
SRPK2	U88666_at	U88666	PASS	8	5.38	PASS	12	8	5.08	1.06	1.06	7q22-q31.1	SFRS protein kinase 2
B2M	S82297_at	S82297	PASS	9	164.00	PASS	13	9	155.15	1.06	1.06	15q21-q22.2	beta-2-microglobulin
SRP54	U51920_at	U51920	PASS	6	5.17	PASS	10	6	4.90	1.05	1.05		signal recognition particle 54kD
U84011_s_at	U84011_s_at	U84011	PASS	5	4.80	PASS	9	5	4.56	1.05	1.05	1p21	amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)
E 23865	U90912_at	U90912	PASS	7	5.71	PASS	7	7	5.43	1.05	1.05		splicing factor, arginine/serine-rich 9
SFRS3	U30825_at	U30825	PASS	9	31.44	PASS	13	9	29.92	1.05	1.05		splicing factor, arginine/serine-rich 9

HNRPH2	U01923_at	PASS	7	6.71	PASS	10	7	6.40	1.05	1.05	RPL14	ribosomal protein L14
RPL14	D87735_at	PASS	9	150.33	PASS	13	9	143.31	1.05	1.05		
W52B f	HG3576-HT3	PASS	9	106.89	PASS	13	9	102.08	1.05	1.05		
AMFR	M63175_at	PASS	5	6.80	PASS	8	5	6.50	1.05	1.05	AMFR	autocrine motility factor receptor
K73_CVCRH	D38552_at	PASS	6	6.83	PASS	13	6	6.54	1.05	1.05	KIAA0073	The hla1539 protein is related to cyclophilin.
MCM3	D38073_at	PASS	8	6.88	PASS	10	8	6.60	1.04	1.04	MCM3	minichromosome maintenance deficient (S. cerevisiae) 3
PAK3	U25975_at	PASS	5	5.60	PASS	10	5	5.40	1.04	1.04	hPAK65	rac/CDC42Hs activated kinase; serine kinase; Method: conceptual translation supplied by author
U67122_s_at	U67122_s_at	PASS	7	11.00	PASS	13	7	10.62	1.04	1.04	SUMO-1	conjugated post-translationally to RanGAP1; ubiquitin-related protein; similar to UBL1 encoded by GenBank Accession Number U38784, PIC1 encoded by GenBank Accession Number U61397 and GMP1 encoded by GenBank Accession Number U72722
L06797_s_at	L06797_s_at	PASS	9	33.67	PASS	13	9	32.54	1.03	1.03	CXCR4	Neuropeptide Y receptor Y3
CAT ma1	X04085_ma1	PASS	7	15.43	PASS	13	7	14.92	1.03	1.03		catase
SFRS3	D28423_at	PASS	6	17.33	PASS	12	6	16.83	1.03	1.03		pre-mRNA splicing factor
J02683_s_at	J02683_s_at	PASS	9	31.56	PASS	13	9	30.69	1.03	1.03	ANT2	adenine nucleotide translocator 2 (fibroblast)
RP57 ma1	Z25749_ma1	PASS	9	136.56	PASS	13	9	132.85	1.03	1.03	RP57	ribosomal protein S7
HDAC2	U31814_at	PASS	9	6.78	PASS	10	9	6.60	1.03	1.03	HDAC2	histone deacetylase 2
M60974_s_a	M60974_s_a	PASS	5	5.60	PASS	10	5	5.50	1.02	1.02	DDIT1	DNA-damage-inducible transcript 1
SEMA	U60800_at	PASS	9	22.22	PASS	13	9	21.85	1.02	1.02	CD100	semaphorin
D13631_s_at	D13631_s_at	PASS	7	11.00	PASS	12	7	10.83	1.02	1.02	KIAA0006	
PRKACB	M34181_at	PASS	5	6.80	PASS	10	5	6.70	1.01	1.01	PRKACB	protein kinase, cAMP-dependent, catalytic, beta
M26730_s_a	M26730_s_a	PASS	9	33.78	PASS	13	9	33.31	1.01	1.01	UQBP	ubiquinone-binding protein (QP)
GD12	D13988_at	PASS	6	18.17	PASS	13	6	18.00	1.01	1.01	GD12	GDP dissociation inhibitor 2
RPL44	M15661_at	PASS	9	51.44	PASS	13	9	51.08	1.01	1.01	RPL44	ribosomal protein L44
ZFPRES24	ZAB000468_a	PASS	8	18.75	PASS	13	8	18.69	1.00	1.00	RNF4	ring finger protein 4
BACTIN5	AFEX-HSAC	PASS	9	240.44	PASS	13	9	240.00	1.00	1.00		
M87507_s_a	M87507_s_a	PASS	6	7.50	PASS	12	6	7.50	1.00	1.00	CASP1	caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)
UVRAG_ma	X99050_ma1	PASS	6	5.00	PASS	11	6	5.00	1.00	1.00	UVRAG	UV radiation resistance associated gene
RP3	U02556_at	PASS	5	6.00	PASS	12	5	6.00	1.00	1.00		RP3 candidate gene
X58528_s_at	X58528_s_at	PASS	5	5.20	PASS	10	5	5.20	1.00	1.00	PMP70	70kDa peroxisomal membrane protein
SFRS3	L10838_at	PASS	8	17.13	PASS	13	8	17.23	0.99	-1.01	SFRS3	splicing factor, arginine/serine-rich 3
METPEP	U29607_at	PASS	9	27.22	PASS	13	9	27.69	0.98	-1.02		methionine aminopeptidase

# Table 1

K253	D87442_at	D87442	PASS	6	8.17	PASS	9	6	8.33	0.98	-1.02	KIAA0253				
CRE3	AFFX-CreX	AFFX-CreX	PASS	9	27.78	PASS	13	9	28.46	0.98	-1.02	UBCH5C	UBCH5C			Transcript is widely expressed. Related to S. Cerevisiae UBC4 and UBC5. Closely related to human UbcH5(A) and to UbcH5B
UBE2D3	U3918_at	U3918	PASS	8	19.00	PASS	13	8	19.54	0.97	-1.03					
U26312_s_at	U26312_s_at	U26312	PASS	6	5.67	PASS	12	6	5.83	0.97	-1.03		HP1HS-gamma			similar to Drosophila heterochromatin protein HP1 Swiss Prot Accession Number P29227, and to human heterochromatin protein HP1HS-alpha encoded by GenBank Accession Number U26311; contains chromo domain; recognized by autoantibodies from some patients with scleroderma; heterochromatin protein
H33B	Z48950_at	Z48950	PASS	9	66.78	PASS	13	9	68.85	0.97	-1.03	H3F3B	histone H3.3	17q25		H3 histone, family 3B (H3.3B)
HNRPF	L28010_at	L28010	PASS	9	14.89	PASS	13	9	15.38	0.97	-1.03	HNRPF	HNRNP F protein	10q11.21		heterogeneous nuclear ribonucleoprotein F
E 23665	U90913_at	U90913	PASS	7	6.00	PASS	10	7	6.20	0.97	-1.03					
YB1	J03827_at	J03827	PASS	9	70.00	PASS	13	9	72.38	0.97	-1.03	YB1		1p34		Major histocompatibility complex, class II, Y box-binding protein I; DNA-binding protein B
ID2B	M96843_at	M96843	PASS	9	7.33	PASS	13	9	7.62	0.96	-1.04	Id2B	contractile protein			
MGC24	D14043_at	D14043	PASS	9	14.22	PASS	13	9	14.77	0.96	-1.04		MGC-24 precursor			
NDUFV3	X99728_at	X99728	PASS	8	8.63	PASS	13	8	9.00	0.96	-1.04					
MTND1	L04490_at	L04490	PASS	7	5.86	PASS	8	7	6.13	0.96	-1.05	NDUFV9	NADH dehydrogenase (ubiquinone)	12p		NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 (39kD)
STATH	U51678_at	U51678	PASS	8	10.88	PASS	13	8	11.38	0.96	-1.05		small acidic protein			
X83416_s_at	X83416_s_at	X83416	PASS	7	6.00	PASS	13	7	6.31	0.95	-1.05	PRNP	prion protein (p27-30) (Creutzfeldt-Jakob disease, Gerstmann-Sträussler-Scheinker syndrome, fatal familial insomnia)	20pter-p12		prion protein (p27-30) (Creutzfeldt-Jakob disease, Gerstmann-Sträussler-Scheinker syndrome, fatal familial insomnia)
UBE2L1	S81003_at	S81003	PASS	9	14.00	PASS	13	9	14.77	0.95	-1.05	UBE2L3	ubiquitin-conjugating enzyme E2L3	22q11.2		ubiquitin-conjugating enzyme E2L3
EIF2A	J02645_at	J02645	PASS	5	7.80	PASS	8	5	8.25	0.95	-1.06	EIF2A	eukaryotic translation initiation factor 2A			eukaryotic translation initiation factor 2A
DLD_ma1	L13761_ma1	L13761	PASS	9	6.67	PASS	12	9	7.08	0.94	-1.06	DLD	dihydropyrimidine dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex)	7q31-q32		dihydropyrimidine dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex)
OCLSF	U63717_at	U63717	PASS	7	7.00	PASS	8	7	7.50	0.93	-1.07		osteoclast stimulating factor			OSF; contains SH3 domain and ankyrin repeat
GNAOI	U01833_at	U01833	PASS	5	5.60	PASS	9	5	6.00	0.93	-1.07	NBP1	nucleotide binding protein 1 (E.coli MinD like)			nucleotide binding protein 1 (E.coli MinD like)

M63838_s_a	M63838_s_a	M63838	PASS	9	12.33	PASS	13	9	13.23	0.93	-1.07	IFI16	lq12-qter	interferon-gamma induced protein	interferon, gamma-inducible protein 16
ADD3	U37122_at	U37122	PASS	7	20.71	PASS	13	7	22.23	0.93	-1.07	ADD3	10q24.2-q24.3	adducin gamma subunit	adducin 3 (gamma)
MLL172	L13773_at	L13773	PASS	9	6.00	PASS	12	9	6.50	0.92	-1.08	AF-4			
Z69030_s_at	Z69030_s_at	Z69030	PASS	7	12.71	PASS	12	7	13.83	0.92	-1.09			gamma 1 isoform of 61kDa regulatory subunit of PP2A	
TIG1_xpt1	U49973_xpt1	U49973	PASS	9	7.56	PASS	13	9	8.23	0.92	-1.09			ORF1; MER37; putative transposase similar to pogo element	
BTAKAP135	U77948_at	U77948	PASS	5	8.40	PASS	13	5	9.15	0.92	-1.09	GTF2I	7q11.23	general transcription factor II, i	general transcription factor II, i
HOU	U32849_at	U32849	PASS	9	10.00	PASS	12	9	10.92	0.92	-1.09	NMI	22q13.3	N-myc (and STAT) interactor	N-myc (and STAT) interactor
KLRB1	HG4263-HT4	HG4263-H1	PASS	9	14.78	PASS	13	9	16.15	0.91	-1.09				
AHNAK	M80899_at	M80899	PASS	7	18.14	PASS	12	7	19.83	0.91	-1.09	AHNAK	11q12-q13	AHNAK nucleoprotein (desmoyokin)	AHNAK nucleoprotein (desmoyokin)
NA	X80909_at	X80909	PASS	9	129.22	PASS	13	9	142.69	0.91	-1.10	alpha NAC		Nascent polypeptide associated complex alpha subunit	
JAK1	M64174_at	M64174	PASS	5	8.80	PASS	13	5	9.85	0.89	-1.12	JAK1	1p32.3-p31.3	Janus kinase 1 (a protein tyrosine kinase)	Janus kinase 1 (a protein tyrosine kinase)
Z48301_s_at	Z48301_s_at	Z48301	PASS	9	113.67	PASS	13	9	127.77	0.89	-1.12	PABPL1	3q22-q25	poly(A)-binding protein-like 1	poly(A)-binding protein-like 1
PRKHT31	HG2167-HT2	HG2167-H1	PASS	5	7.00	PASS	9	5	7.89	0.89	-1.13				
K192_MOP4	D83783_at	D83783	PASS	6	6.00	PASS	13	6	6.77	0.89	-1.13	TRAP230	Xq13	thyroid hormone receptor-associated protein, 230 kDa subunit	thyroid hormone receptor-associated protein, 230 kDa subunit
PRF1	M31951_at	M31951	PASS	6	23.33	PASS	12	6	26.67	0.88	-1.14	PRF1	10q22	perforin 1 (preforming protein)	perforin 1 (preforming protein)
PSMC2	D11094_at	D11094	PASS	7	9.71	PASS	12	7	11.17	0.87	-1.15	PSMC2	7q22.1-q22.3	proteasome (prosome, macropain) 26S subunit, ATPase, 2	proteasome (prosome, macropain) 26S subunit, ATPase, 2
SDHB	U17886_at	U17886	PASS	5	8.00	PASS	12	5	9.25	0.86	-1.16	sdhB		succinate dehydrogenase iron-protein subunit B	
M21119_s_a	M21119_s_a	M21119	PASS	8	59.00	PASS	13	8	69.15	0.85	-1.17			lysosome precursor (EC 3.2.1.17)	lysosome precursor (EC 3.2.1.17)
S311125	L40397_at	L40397	PASS	9	10.78	PASS	13	9	12.77	0.84	-1.18			ORF; putative	ORF; putative
RNA566	U64998_at	U64998	PASS	6	13.33	PASS	10	6	15.80	0.84	-1.19			ribonuclease k6 precursor	ribonuclease k6 precursor
IK	S74221_at	S74221	PASS	8	10.13	PASS	12	8	12.08	0.84	-1.19	IK	2p15-p14	IK cytokine, down-regulator of HLA II	IK cytokine, down-regulator of HLA II
U73477_s_at	U73477_s_at	U73477	PASS	6	6.00	PASS	10	6	7.20	0.83	-1.20			acidic nuclear phosphoprotein pp32	LAMP; PHAPI; I-1pp2a
M97796_s_a	M97796_s_a	M97796	PASS	6	17.83	PASS	13	6	21.62	0.83	-1.21	ID2	2p25	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
NIP2	U15173_at	U15173	PASS	8	4.88	PASS	12	8	5.92	0.82	-1.21	BNIP2		BCL2/adenovirus E1B 19kD-interacting protein 2	BCL2/adenovirus E1B 19kD-interacting protein 2
POLR2B	X63563_at	X63563	PASS	7	6.71	PASS	12	7	8.17	0.82	-1.22	POLR2B	4q12	polymerase (RNA) II (DNA directed) polypeptide B (140kD)	polymerase (RNA) II (DNA directed) polypeptide B (140kD)
AFFX-CreX	AFFX-CreX	AFFX-CreX	PASS	8	15.38	PASS	13	8	18.77	0.82	-1.22				
TRAMP	X63679_at	X63679	PASS	6	8.50	PASS	13	6	10.38	0.82	-1.22	TRAM		TRAM protein	
SAP18	U96915_at	U96915	PASS	8	13.13	PASS	13	8	16.08	0.82	-1.22	SAP18		sin3 associated polypeptide p18	SAP18p
BIOC5	AFFX-BioC	AFFX-BioC	PASS	9	16.00	PASS	13	9	19.62	0.82	-1.23				
RBI	HG4036-HT4	HG4036-H1	PASS	8	11.13	PASS	13	8	14.31	0.78	-1.29				
TFA	L06633_at	L06633	PASS	8	6.75	PASS	13	8	8.85	0.76	-1.31	HE	2	cytohesin binding protein HE	cytohesin binding protein HE
IL7R	M29696_at	M29696	PASS	8	26.38	PASS	11	8	34.73	0.76	-1.32	IL7R	5p13	interleukin 7 receptor	interleukin 7 receptor

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ZFP20	HG3454-HTT	HG3454-H	PASS	7	5.43	PASS	9	7	7.22	0.75	-1.33					
COPB	X70476_at	X70476	PASS	8	6.38	PASS	13	8	8.92	0.71	-1.40	COPB2	3q23	coatmer protein complex, subunit beta 2 (beta prime)	coatmer protein complex, subunit beta 2 (beta prime)	
RAP1B	HG3521-HTT	HG3521-H	PASS	9	17.56	PASS	13	9	25.62	0.69	-1.46					
BIOB3	AFFX-BioB-1	AFFX-BioB	PASS	9	27.11	PASS	13	9	39.77	0.68	-1.47					
PROGBP	Y12711_at	Y12711	PASS	6	9.33	PASS	13	6	14.00	0.67	-1.50			putative progesterone binding protein		
M27394_s_a1	M27394_s_a1	M27394	PASS	6	6.00	PASS	11	6	9.73	0.62	-1.62			cell surface antigen B1		
DAP3	AFFX-DapX	AFFX-Dap	PASS	9	6.56	PASS	13	9	10.69	0.61	-1.63					
M14483_ma	M14483_ma	M14483	PASS	9	65.89	PASS	13	9	109.31	0.60	-1.66	PTMA	2	prothymosin, alpha (gene sequence 28)	prothymosin, alpha (gene sequence 28)	
BIOD3	AFFX-BioDn	AFFX-BioD	PASS	9	29.56	PASS	13	9	65.62	0.45	-2.22					

## 6800 human RA Phosphatase and kinase list

name	qualifier	GeneSpring qualifier	Patients		Normals		#"p" (Normal)	#"p" (RA)	Avg Freq Normals	Ratio	Fold Change	Symbol	Chromosome	Description	Kinase or Phosphatase
			called "p">4	called "p">6	Avg Freq - RA Patients	called "p">6									
Kinases															
RAC2	M64595_at		fail	3		PASS	13	3	19.85	Normal	Normal	RAC2	22q12-q13.2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	Kinase
FRAP	L34075_at		fail	1		PASS	11	1	5.73	Normal	Normal	FRAP1	1p36.2	FKBP-rapamycin associated protein	Kinase
CAMK2A	U81554_at		fail	1		PASS	10	1	5.50	Normal	Normal	CAMK2G	10q22	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	Kinase
CDK7	L20320_at		fail	1		PASS	9	1	4.89	Normal	Normal	CDK7	2p15-cen	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	Kinase
EPHB4	U07695_at		fail	0		PASS	8	0	6.50	Normal	Normal	EPHB4	7	EphB4	Kinase
PRP4H	U48736_at		fail	0		PASS	8	0	5.00	Normal	Normal	PRP4		serine/threonine-protein kinase PRP4 homolog	Kinase
BLK	S76617_at		fail	0		PASS	7	0	4.71	Normal	Normal	BLK	8p23-p22	B lymphoid tyrosine kinase	Kinase
CHED	M80629_at		fail	3		PASS	10	3	5.30	Normal	Normal	CDC2L		cholesterase-related cell division controller	Kinase
CLC	L01664_at		fail	3		PASS	9	3	7.22	Normal	Normal	CLC	19q13.1	Charot-Leyden crystal protein	Kinase
L05624_s	L05624_s_at		fail	3		PASS	9	3	5.56	Normal	Normal			MAP kinase kinase	Kinase
PLK	U01038_at		fail	3		PASS	9	3	5.56	Normal	Normal			pLK	Kinase
S80267_s	S80267_s_at		fail	4		PASS	8	4	4.88	Normal	Normal	p72syk		p72syk	Kinase
CSNK1A1	L37042_at		fail	4		PASS	7	4	8.00	Normal	Normal	CSNK1A1	13q13	casein kinase 1, alpha 1	Kinase
CSNK2A1	M55265_at		fail	3		PASS	7	3	5.86	Normal	Normal	CSNK2A1	20p13	casein kinase 2, alpha 1 polypeptide	Kinase
HG4120-HT	HG4120-HT		PASS	6	5.17	fail	3	6		Disease	Disease			leukocyte tyrosine kinase	Kinase
LTK	D16105_at		PASS	9	23.78	fail	3	9		Disease	Disease	LTK	15		Kinase
K60_GNP	D31766_at		PASS	8	14.50	fail	6	8		Disease	Disease	KIAA0060		KIAA0060 gene product	Kinase
CDK2	M68520_at		PASS	8	7.63	fail	6	8		Disease	Disease	CDK2	12q13	cyclin-dependent kinase 2	Kinase
PRKACG	M34182_at		PASS	8	41.00	fail	5	8		Disease	Disease	PRKACG	9q13	protein kinase, cAMP-dependent, catalytic, gamma	Kinase
K213	D86968_at		PASS	7	4.14	fail	6	7		Disease	Disease	KIAA0213		Similar to Mouse TFIIi-associated transactivator factor p17(GB_ROMMU11548): Containing protein kinase motif	Kinase
TESK1	D50863_at		PASS	5	8.80	fail	6	5		Disease	Disease	TESK1	9p13	TESK1 testis-specific kinase 1	Kinase
GCDH	U69141_at		PASS	5	6.40	fail	4	5		Disease	Disease	GCDH	19p13.2	glutaryl-Coenzyme A dehydrogenase	Kinase
ILK	U40282_at		PASS	9	29.22	PASS	12	9	8.58	3.40	3.40	ILK	11p15.5-p15.4	integrin-linked kinase	Kinase
HCF1	L20010_at		PASS	8	26.13	PASS	13	8	8.92	2.93	2.93				Kinase
PRKMK3	D87116_at		PASS	9	32.89	PASS	11	9	11.27	2.92	2.92	PRKMK3	17q11.2	protein kinase, mitogen-activated, kinase 3 (MAP kinase kinase 3)	Kinase
FAST	X86779_at		PASS	9	20.33	PASS	10	9	7.30	2.79	2.79	fast		PAST kinase	Kinase
X59932_s	X59932_s_at		PASS	9	62.44	PASS	13	9	22.46	2.78	2.78	CSK	15q23-q25	c-src tyrosine kinase	Kinase
CSNK2A2	M55268_at		PASS	9	17.33	PASS	7	9	6.57	2.64	2.64	CSNK2A2	16p13.3-p13.2	casein kinase 2, alpha prime polypeptide	Kinase

K151_SPK	D63485 at	D63485	PASS	9	18.89	PASS	10	9	7.20	2.62	2.62	KIAA0151	6p21.1	KIAA0151 gene product	Kinase
M16750_s	M16750_s at	M16750	PASS	9	34.89	PASS	13	9	13.92	2.51	2.51	PIM1	6p21.1	pim-1 oncogene	Kinase
RPS6KA2	L07597 at	L07597	PASS	9	28.78	PASS	12	9	11.92	2.41	2.41	RPS6KA1	3	ribosomal protein S6 kinase, 90kD, polypeptide 1	Kinase
ECGF1_m	U62317_m	U62317	PASS	9	66.22	PASS	13	9	27.54	2.40	2.40			arylsulfatase A	Kinase
GLA	X14448 at	X14448	PASS	9	20.56	PASS	13	9	8.62	2.39	2.39			alpha-D-galactosidase A	Kinase
DGK5Z	U51477 at	U51477	PASS	9	32.56	PASS	13	9	13.77	2.36	2.36	DGKZ		diacylglycerol kinase, zeta (104kD)	Kinase
PIM2	U77735 at	U77735	PASS	6	24.33	PASS	12	6	10.33	2.35	2.35			pim-2 protooncogene homolog pim-2h	Kinase
M54915_s	M54915_s at	M54915	PASS	9	54.67	PASS	13	9	23.54	2.32	2.32			pim-1 protein	Kinase
CAKB	U43522 at	U43522	PASS	8	14.13	PASS	9	8	6.11	2.31	2.31	PTK2B	8p21.1	focal adhesion kinase 2 (protein kinase B)	Kinase
M13829_s	M13829_s at	M13829	PASS	8	15.25	PASS	13	8	6.69	2.28	2.28	ARAF1	Xp11.4-p11.2	v-rat murine sarcoma 3611 viral oncogene homolog 1	Kinase
AKT1	M63167 at	M63167	PASS	8	23.13	PASS	11	8	10.18	2.27	2.27	AKT1	14q32.3	rac protein kinase-alpha	Kinase
ZAP70	L05148 at	L05148	PASS	9	36.56	PASS	13	9	16.31	2.24	2.24				Kinase
RAD23A	D21235 at	D21235	PASS	9	15.56	PASS	10	9	7.00	2.22	2.22	RAD23A	19p13.2	HHR23A protein, RAD23 (S. cerevisiae) homolog A	Kinase
FGFR	M19722 at	M19722	PASS	9	94.78	PASS	13	9	43.00	2.20	2.20	FGFR	1p36.2-p36.1	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog	Kinase
DAGK1	X62535 at	X62535	PASS	9	38.56	PASS	13	9	17.92	2.15	2.15	DGKA	12	diacylglycerol kinase	Kinase
C8FWPH	AJ000480 at	AJ000480	PASS	5	11.60	PASS	9	5	5.44	2.13	2.13	C8FW		phosphoprotein	Kinase
D63479_s	D63479_s at	D63479	PASS	9	18.67	PASS	12	9	8.83	2.11	2.11	DGKD		diacylglycerol kinase, delta (130kD)	Kinase
HPK1	U66464 at	U66464	PASS	9	16.89	PASS	13	9	8.00	2.11	2.11	HPK1		hematopoietic progenitor kinase	Kinase
GPRK6	L16862 at	L16862	PASS	7	25.29	PASS	7	7	12.00	2.11	2.11	GPRK6	5q35	G protein-coupled receptor kinase 6	Kinase
IRAK1	L76191 at	L76191	PASS	9	32.67	PASS	13	9	15.54	2.10	2.10	IRAK1	Xq28	interleukin-1 receptor-associated kinase 1	Kinase
PI4KB	U81802 at	U81802	PASS	7	14.71	PASS	11	7	7.00	2.10	2.10	PIK4CB	1q21	phosphatidylinositol 4-kinase, catalytic, beta polypeptide	Kinase
Z69043_s	Z69043_s at	Z69043	PASS	9	57.11	PASS	13	9	27.62	2.07	2.07	H-TRAP delta		translocin-associated protein delta subunit precursor	Kinase
GSK3A	L40027 at	L40027	PASS	9	19.89	PASS	13	9	9.77	2.04	2.04			glycogen synthase kinase 3	Kinase
PIK4	L36151 at	L36151	PASS	9	39.89	PASS	13	9	19.69	2.03	2.03	PIK4CA		phosphatidylinositol 4-kinase, catalytic, alpha polypeptide	Kinase
3PK	U09578 at	U09578	PASS	8	17.25	PASS	13	8	8.54	2.02	2.02	MAPKAPK3	3p21.3	mitogen-activated protein kinase-activated protein kinase 3	Kinase
MLK3	L32976 at	L32976	PASS	7	12.29	PASS	7	7	6.14	2.00	2.00	MLK3	11q13.1-q13.3	mixed lineage kinase 3	Kinase
CLK2	L29218 at	L29218	PASS	7	13.71	PASS	11	7	7.09	1.93	1.93	CLK2	1q21	CDC-like kinase 2	Kinase
K135_PIM	D50925 at	D50925	PASS	6	12.00	PASS	9	6	6.33	1.89	1.89	KIAA0135		The KIAA0135 gene is related to pim-1 oncogene.	Kinase
ZAP112	L40399 at	L40399	PASS	6	26.50	PASS	10	6	14.00	1.89	1.89			ORF, putative	Kinase
CBGOS39	D87119 at	D87119	PASS	8	19.75	PASS	12	8	10.50	1.88	1.88	GS955		GS955	Kinase
PRKCD	D10495 at	D10495	PASS	9	30.22	PASS	12	9	16.58	1.82	1.82			protein kinase C delta-type	Kinase
CSNK1D	U29171 at	U29171	PASS	9	18.22	PASS	12	9	10.08	1.81	1.81	CSNK1D	17q25	casein kinase I, delta	Kinase
K96_PK	D43636 at	D43636	PASS	9	15.89	PASS	13	9	9.00	1.77	1.77	KIAA0096		KIAA0096 gene product is related to a protein kinase.	Kinase
FYN	M14676 at	M14676	PASS	9	31.89	PASS	13	9	18.08	1.76	1.76	FYN	6q21	FYN oncogene related to SRC, FGR, YES	Kinase
CSNK1G2	U89896 at	U89896	PASS	6	9.83	PASS	9	6	5.67	1.74	1.74			casein kinase I gamma 2	Kinase



TRNA5TL	U07424_at	U07424	PASS	7	14.00	PASS	11	7	8.09	1.73	1.73	FARSL		phenylalanine-tRNA synthetase-like	Kinase
PKUA	AB004884_s	AB004884	PASS	7	12.29	PASS	8	7	7.13	1.72	1.72			PKU-alpha	Kinase
U23852_s	U23852_s	U23852	PASS	9	66.89	PASS	13	9	38.85	1.72	1.72	lek		p50ck	Kinase
DYRK	D86550_at	D86550	PASS	9	18.67	PASS	13	9	10.85	1.72	1.72	hMNB		serine/threonine protein kinase	Kinase
SLC6A8_m	U36341_ma	U36341	PASS	9	13.11	PASS	9	9	7.67	1.71	1.71	SLC6A8		creatine transporter	Kinase
SSBP	M94556_at	M94556	PASS	9	23.78	PASS	13	9	14.15	1.68	1.68	SSBP	7q34	single-stranded DNA-binding protein	Kinase
D13720_s	D13720_s	D13720	PASS	8	14.25	PASS	13	8	8.62	1.65	1.65			ITK	Kinase
ABR	U01147_at	U01147	PASS	9	9.89	PASS	12	9	6.00	1.65	1.65	ABR	17p13.3	guanine nucleotide regulatory protein	Kinase
M16591_s	M16591_s	M16591	PASS	9	29.44	PASS	13	9	17.92	1.64	1.64	HCK	20q11-q12	hemopoietic cell kinase	Kinase
X77588_s	X77588_s	X77588	PASS	8	10.88	PASS	12	8	6.67	1.63	1.63	ARD1	Xq28	ARD1 N-acetyl transferase homologue	Kinase
TFE3_ma	X97160_ma	X97160	PASS	7	9.29	PASS	7	7	6.00	1.55	1.55			TFE3 transcription factor	Kinase
M30448_s	M30448_s	M30448	PASS	9	58.11	PASS	13	9	38.38	1.51	1.51	CSNK2B	6p21-p12	casein kinase 2, beta polypeptide	Kinase
K137_COS	D50927_at	D50927	PASS	8	10.25	PASS	13	8	6.85	1.50	1.50	KIAA0137		KIAA0137 gene product	Kinase
PAK1	U24152_at	U24152	PASS	9	13.22	PASS	12	9	8.83	1.50	1.50	PAK1	11q13-q14	p21/Cdc42/Rac1-activated kinase 1 (yeast Ste20-related)	Kinase
ZPK	U07358_at	U07358	PASS	7	8.86	PASS	11	7	6.09	1.45	1.45	ZPK	12q13	serine/threonine protein kinase	Kinase
PSMB10_c	X71874_cds	X71874	PASS	9	73.89	PASS	13	9	51.23	1.44	1.44	PSMB10	16q22.1	proteasome (prosome, macropain) subunit, beta type, 10	Kinase
M36430_s	M36430_s	M36430	PASS	7	12.71	PASS	13	7	8.85	1.44	1.44	GNB1	1p36.21-36.33	guanine nucleotide binding protein (G protein), beta polypeptide 1	Kinase
RP56KA2	U08316_at	U08316	PASS	5	8.00	PASS	11	5	5.64	1.42	1.42	RP56KA3	Xp22.2-p22.1	ribosomal protein S6 kinase, 90kD, polypeptide 3	Kinase
ATP7A	AB000409_a	AB000409	PASS	9	9.89	PASS	10	9	7.10	1.39	1.39	MKNK1		MAP kinase-interacting serine/threonine kinase 1	Kinase
HG3730-HT	HG3730-HT	HG3730-HT	PASS	8	9.75	PASS	12	8	7.08	1.38	1.38			v-src-1 Yamaguchi sarcoma viral related oncogene homolog	Kinase
LYN	M16038_at	M16038	PASS	9	17.11	PASS	13	9	12.54	1.36	1.36	LYN	8q13		Kinase
D26535_s	D26535_s	D26535	PASS	8	10.00	PASS	11	8	7.36	1.36	1.36	DLST	14q24.3	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	Kinase
DYRK2	Y09216_at	Y09216	PASS	6	10.17	PASS	12	6	7.50	1.36	1.36	DYRK2	12	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	Kinase
BTX_ma	U78027_ma	U78027	PASS	7	10.71	PASS	12	7	7.92	1.35	1.35	FTP3		FTP3	Kinase
PSKH1	U09564_at	U09564	PASS	8	7.50	PASS	11	8	5.55	1.35	1.35	SRPK1	6p21.2-p21.3	SFRS protein kinase 1	Kinase
VRK1	AB000449_a	AB000449	PASS	7	7.57	PASS	10	7	5.90	1.28	1.28	VRK1	14q32	vaccinia related kinase 1	Kinase
HNRNPCL	M94630_at	M94630	PASS	9	27.56	PASS	13	9	21.69	1.27	1.27	HNRPD	4q21	heterogeneous nuclear ribonucleoprotein D	Kinase
TGFB2	D50683_at	D50683	PASS	9	24.00	PASS	13	9	18.92	1.27	1.27	TGFB2	3p22	transforming growth factor, beta receptor II (70-80kD)	Kinase
GPRK5	L15388_at	L15388	PASS	6	6.33	PASS	7	6	5.00	1.27	1.27	GPRK5	10q24-qter	G protein-coupled receptor kinase	Kinase
HG3484-HT	HG3484-HT	HG3484-HT	PASS	7	8.86	PASS	12	7	7.00	1.27	1.27				Kinase

# Phosphatase

ATM	U33841_at	U33841	PASS	5	6.20	PASS	9	5	5.11	1.21	1.21	ATM	11q22-q23	ataxia telangiectasia mutated (includes complementation groups A, C and D)	Kinase
DNAPKCS	U47077_at	U47077	PASS	7	5.29	PASS	8	7	4.38	1.21	1.21	PRKDC	8q11	DNA-dependent protein kinase catalytic subunit	Kinase
YES1	M15990_at	M15990	PASS	7	5.43	PASS	7	7	4.71	1.15	1.15	YES1	18p11.31-p11.21	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	Kinase
PRKMK1	L11284_at	L11284	PASS	7	10.29	PASS	13	7	9.46	1.09	1.09	PRKMK1	15q22.1-q22.33	protein kinase, mitogen-activated, kinase 1 (MAP kinase kinase 1)	Kinase
S203_15	L40395_at	L40395	PASS	8	6.50	PASS	9	8	6.11	1.06	1.06	SRPK2	7q22-q31.1	ORF, putative	Kinase
SRPK2	U88666_at	U88666	PASS	8	5.38	PASS	12	8	5.08	1.06	1.06	SRPK2	7q22-q31.1	SRFS protein kinase 2	Kinase
PAK3	U25975_at	U25975	PASS	5	5.60	PASS	10	5	5.40	1.04	1.04	HPAK65		HPAK65	Kinase
PRKACB	M34181_at	M34181	PASS	5	6.80	PASS	10	5	6.70	1.01	1.01	PRKACB	1	protein kinase, cAMP-dependent, catalytic, beta	Kinase
JAK1	M64174_at	M64174	PASS	5	8.80	PASS	13	5	9.85	0.89	-1.12	JAK1	1p32.3-p31.3	Janus kinase 1 (a protein tyrosine kinase)	Kinase

Phosphatases															
PTPRA	M34668_at	M34668	fail	2		PASS	9	2	5.67	Normal	Normal	PTPRA	20p13	protein tyrosine phosphatase, receptor type, alpha polypeptide	Phosphatase
PTEN	U92436_at	U92436	fail	3		PASS	11	3	5.00	Normal	Normal	PTEN	10q23	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	Phosphatase
PLCD1	U09117_at	U09117	fail	4		PASS	7	4	7.57	Normal	Normal			phospholipase c delta 1	Phosphatase
PTPRE	HG620-HT6	HG620-HT6	fail	3		PASS	7	3	8.00	Normal	Normal				Phosphatase
PLCG2H	U45974_at	U45974	PASS	5	15.40	fail	0	5		Disease	Disease				Phosphatase
PTPRN	L18983_at	L18983	PASS	5	20.00	fail	0	5		Disease	Disease	PTPRN	2q35-q36.1	protein tyrosine phosphatase, receptor type, N	Phosphatase
INPPL1	L36818_at	L36818	PASS	7	21.71	fail	6	7		Disease	Disease			S1C protein	Phosphatase
M33684_s	M33684_s_at	M33684	PASS	5	6.60	fail	3	5		Disease	Disease	PTPN1		non-receptor tyrosine phosphatase 1	Phosphatase
PLCB2	M95678_at	M95678	PASS	9	84.00	PASS	12	9	26.92	3.12	3.12	PLCB2	15q15	phospholipase C, beta 2	Phosphatase
K15_PPM1D	D13640_at	D13640	PASS	9	29.00	PASS	12	9	11.33	2.56	2.56	KIAA0015			Phosphatase
PPP4C	X70218_at	X70218	PASS	7	27.43	PASS	11	7	11.18	2.45	2.45	PPP4C	16p12-16p11	protein phosphatase 4 (formerly X), catalytic subunit	Phosphatase
INPP5D	U57650_at	U57650	PASS	9	42.78	PASS	13	9	18.77	2.28	2.28	INPP5D	2q36-q37	SH2-containing inositol 5-phosphatase	Phosphatase
PP1	U14603_at	U14603	PASS	9	76.56	PASS	13	9	35.31	2.17	2.17	PTP4A2	1p35	protein tyrosine phosphatase type IVA, member 2	Phosphatase
J03805_s	J03805_s_at	J03805	PASS	9	14.33	PASS	13	9	7.23	1.98	1.98	PPP2CB	8p12-p11.2	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	Phosphatase
M37238_s	M37238_s_at	M37238	PASS	9	11.33	PASS	9	9	6.22	1.82	1.82	PLCO2	16q24.1	phospholipase C, gamma 2 (phosphatidylinositol-specific)	Phosphatase
PTPCAAX	U48296_at	U48296	PASS	7	8.43	PASS	8	7	5.13	1.64	1.64	PTP4A1	6q12	Protein tyrosine phosphatase IVA1	Phosphatase

# Phosphatase

PPP3CB	S46622_at	S46622	PASS	5	6.40	PASS	10	5	4.40	1.45	1.45	calcineurin A catalytic subunit, calmodulin-dependent protein phosphatase catalytic subunit, CaM-	7q11.23	calcineurin A catalytic subunit	Phosphatase
PTPN12	M93425_at	M93425	PASS	9	16.22	PASS	13	9	11.69	1.39	1.39	PTPN12	7q11.23	protein tyrosine phosphatase, non-receptor type 12	Phosphatase
PPP3CB2	M29551_at	M29551	PASS	5	7.60	PASS	9	5	6.00	1.27	1.27				Phosphatase
PTPN4	M68941_at	M68941	PASS	7	7.86	PASS	9	7	6.56	1.20	1.20	PTPN4		protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte)	Phosphatase
ACP1	U25849_at	U25849	PASS	6	9.83	PASS	13	6	8.69	1.13	1.13	ACP1	2p25	acid phosphatase 1, soluble	Phosphatase
M60483_mt	M60483_ma	M60483	PASS	8	6.50	PASS	12	8	5.75	1.13	1.13	PPP2CA	5q23-q31	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	Phosphatase
D11327_s	D11327_s_a	D11327	PASS	8	5.75	PASS	10	8	5.10	1.13	1.13	PTPN7	1q32.1	protein tyrosine phosphatase, non-receptor type 7	Phosphatase
PPM1A	S87759_at	S87759	PASS	7	6.00	PASS	9	7	5.33	1.13	1.13	PPM1B		protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform	Phosphatase

Table 3

Human RA PBMC data on U95

Human RA PBMC data on U95																
Atty Qualifier	Atty Name	accession	sum of Present Cells	4 of 6 present	RA	Avg Freq Std Dev	7 of 13 present	Present in RA and Normal	Present in RA, Absent in Normal	Absent in RA, Present in Normal	Avg Freq (Normal)	Fold Change RA / Normal	Name	Chromosome	Kinase or Phosphatase	
Kinases										Normal						
446_at	CSNK1G2	U89896	6	Pass	9.17	3.54	13	Pass	TRUE	FALSE	FALSE	4.69	1.95	casein kinase 1, gamma 2; CSNK1G2	19p13.3	Kinase
490_g_at	MUTYH	U63329	6	Pass	11.00	2.97	13	Pass	TRUE	FALSE	FALSE	5.62	1.96	mutY (E. coli) homolog; MUTYH	1p34.3-p32.1	Kinase
41197_at	RAD23A	D21235	6	Pass	18.50	4.32	13	Pass	TRUE	FALSE	FALSE	9.38	1.97	RAD23 (S. cerevisiae) homolog A; RAD23A	19p13.2	Kinase
33300_at	CDC2L1	AL031282	6	Pass	11.83	3.76	12	Pass	TRUE	FALSE	FALSE	5.92	2.00	Human Inel AL031282: Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, and GSSs. <i>complete sequence</i>		Kinase
40742_at	HCK	M16591	6	Pass	52.50	31.65	13	Pass	TRUE	FALSE	FALSE	25.92	2.03	hemopoietic cell kinase; <i>HCK</i>	20q11-q12	Kinase
32799_at	CIORF2	AF023268	6	Pass	24.17	6.43	11	Pass	TRUE	FALSE	FALSE	11.91	2.03	secretory carrier membrane protein 3; <i>HCK</i>		Kinase
1622_at	MAP2K3	D87116	6	Pass	40.17	14.39	13	Pass	TRUE	FALSE	FALSE	19.77	2.03	mitogen-activated protein kinase kinase 3; MAP2K3	17q11.2	Kinase
146_at	PIK4CB	U81802	6	Pass	6.33	1.75	9	Pass	TRUE	FALSE	FALSE	3.11	2.04	phosphatidylinositol 4-kinase, catalytic, beta polypeptide; PIK4CB	1q21	Kinase
1392_at	GPRK6	L16862	4	Pass	28.25	5.50	7	Pass	TRUE	FALSE	FALSE	13.86	2.04	G protein-coupled receptor kinase 6; GPRK6	5q35	Kinase
33314_at	GCDH	U69141	6	Pass	6.17	1.17	11	Pass	TRUE	FALSE	FALSE	3.00	2.06	glutaryl-Coenzyme A dehydrogenase; GCDH	19p13.2	Kinase
34808_at	KIAA0999	AB023216	6	Pass	12.50	2.51	13	Pass	TRUE	FALSE	FALSE	6.08	2.06	KIAA0999 protein; KIAA0999		Kinase
32046_at	PRKCD	D10495	6	Pass	26.83	9.93	13	Pass	TRUE	FALSE	FALSE	13.00	2.06	protein kinase C, delta; PRKCD	3p	Kinase
384_at	PSMB10	X71874	6	Pass	50.00	22.63	13	Pass	TRUE	FALSE	FALSE	24.15	2.07	proteasome (prosome, macropain) subunit, beta type, 10; PSMB10	16q22.1	Kinase
41249_at	UNK_AL0	AL031282	6	Pass	25.67	13.23	13	Pass	TRUE	FALSE	FALSE	12.31	2.09			Kinase
32716_at	DGKA	X62555	6	Pass	46.33	9.56	13	Pass	TRUE	FALSE	FALSE	22.08	2.10	diacylglycerol kinase, alpha (80kD); DGKA	12q13.3	Kinase
1779_s_at	PIM1	M16750	6	Pass	42.00	9.61	13	Pass	TRUE	FALSE	FALSE	20.00	2.10	p115 oncogene; PIM1	6p21.2	Kinase
31873_at	ARDJ	U52112	6	Pass	8.67	2.50	11	Pass	TRUE	FALSE	FALSE	4.09	2.12	mitogen-activated protein kinase kinase	11q13	Kinase
187_at	MAP4K2	U07349	5	Pass	5.80	1.30	7	Pass	TRUE	FALSE	FALSE	2.71	2.14	kinase kinase kinase 2; MAP4K2		Kinase
37910_at	HCFCl	U52112	6	Pass	8.17	3.60	11	Pass	TRUE	FALSE	FALSE	3.82	2.14	host cell factor C1 (VP16 accessory protein); Gardier-Rasheed feline sarcoma viral (v-fgr) oncogene homolog; FGR	Xq28	Kinase
1780_at	FGR	M19722	6	Pass	80.83	35.22	13	Pass	TRUE	FALSE	FALSE	37.77	2.14	IKK-related kinase epsilon; inducible IkappaB kinase; IKKE	1p36.2-p36.1	Kinase
33281_at	KIAA0151	D63485	6	Pass	14.33	1.63	13	Pass	TRUE	FALSE	FALSE	6.69	2.14	diacylglycerol kinase, delta (130kD); DGKD		Kinase
39044_s_at	DGKD	D73409	6	Pass	31.67	7.76	13	Pass	TRUE	FALSE	FALSE	14.77	2.14	serine/threonine kinase 10; STK10	5q35.1	Kinase
40420_at	STK10	AB015718	6	Pass	35.17	8.70	13	Pass	TRUE	FALSE	FALSE	16.38	2.15	cyclin G associated kinase; GAK	4p16	Kinase
40225_at	GAK	D88435	6	Pass	37.17	12.67	13	Pass	TRUE	FALSE	FALSE	17.31	2.15	glycogen synthase kinase-3 alpha; GSK3A		Kinase
632_at	GSK3A	L40027	6	Pass	19.00	5.69	13	Pass	TRUE	FALSE	FALSE	8.77	2.17			Kinase

Human RA 2x or greater

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Ally Qualifier	Ally Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of abs dec	Present in RA and Normal	Present In RA, Absent in Normal	Absent in RA, Present in Normal	Avg Freq (Normal) RA / Normal	Fold Change RA / Normal	Name	Chromosome	Kinase or Phosphatase
35796_at	PTK9L	Y17169	6	Pass	16.17	9.54	12	Pass	TRUE	FALSE	7.42	2.18	protein tyrosine kinase 9-like (A6-related protein); PTK9L	3p21.1	Kinase
2075_s_at	MAP2K3	L36719	6	Pass	17.67	4.23	12	Pass	TRUE	FALSE	8.00	2.21	mitogen-activated protein kinase kinase 3; MAP2K3	17q11.2	Kinase
33301_g_at	CDC2L1	AL031282	6	Pass	21.50	7.34	13	Pass	TRUE	FALSE	9.69	2.22	Cluster Inc1 AL031282: Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract		Kinase
1810_s_at	PRKCD	D10495	6	Pass	14.00	5.62	11	Pass	TRUE	FALSE	6.27	2.23	protein kinase C, delta; PRKCD	3p	Kinase
36949_at	CSNK1D	U29171	6	Pass	45.00	11.93	13	Pass	TRUE	FALSE	20.08	2.24	casein kinase 1, delta; CSNK1D	17q25	Kinase
1707_g_at	ARAF1	U01337	6	Pass	31.00	6.75	11	Pass	TRUE	FALSE	13.82	2.24	v-rat murine sarcoma 3611 viral oncogene homolog 1; ARAF1 Ser/Thr protein kinase	Xp11.4-p11.2	Kinase
38617_at	LIMK2	D45906	5	Pass	9.00	2.55	11	Pass	TRUE	FALSE	4.00	2.25	LIM domain kinase 2; LIMK2	22q12.2	Kinase
35299_at	MKNK1	AB000409	6	Pass	8.67	2.73	12	Pass	TRUE	FALSE	3.83	2.26	MAP kinase-interacting serine/threonine kinase 1; MKNK1		Kinase
34291_at	FARSL	U07424	6	Pass	11.00	3.35	13	Pass	TRUE	FALSE	4.77	2.31	phenylalanine-tRNA synthetase-like; FARSL	19p13.2	Kinase
1498_at	ZAP70	L05148	6	Pass	35.67	9.71	13	Pass	TRUE	FALSE	15.38	2.32	zeta-chain (TCR) associated protein kinase (70 kD); ZAP70	2q12	Kinase
1706_at	ARAF1	U01337	6	Pass	25.17	6.43	13	Pass	TRUE	FALSE	10.69	2.35	v-rat murine sarcoma 3611 viral oncogene homolog 1; ARAF1	Xp11.4-p11.2	Kinase
1127_at	RPS6KA1	L07597	6	Pass	33.67	13.82	13	Pass	TRUE	FALSE	14.15	2.38	ribosomal protein S6 kinase, 90kD, polypeptide 1; RPS6KA1	3	Kinase
36179_at	MAPKAP2	U12779	6	Pass	36.67	8.19	13	Pass	TRUE	FALSE	15.31	2.40	mitogen-activated protein kinase-activated protein kinase 2; MAPKAPK2		Kinase
1652_at	PIM2	U77735	6	Pass	17.50	7.82	11	Pass	TRUE	FALSE	7.27	2.41	pim-2 oncogene; PIM2	X	Kinase
883_s_at	PIM1	M50915	6	Pass	59.00	8.44	13	Pass	TRUE	FALSE	24.46	2.41	pim-1 oncogene; PIM1	X	Kinase
33804_at	PTK2B	U43522	6	Pass	16.67	7.63	8	Pass	TRUE	FALSE	6.88	2.42	protein tyrosine kinase 2 beta; PTK2B	8p21.1	Kinase
403_at	CSNK1D	U29171	6	Pass	17.17	6.43	13	Pass	TRUE	FALSE	7.08	2.43	casein kinase 1, delta; CSNK1D	17q25	Kinase
1398_g_at	MAP3K11	L32976	6	Pass	27.83	17.62	13	Pass	TRUE	FALSE	11.46	2.43	mitogen-activated protein kinase kinase kinase 11; MAP3K11	11q13.1-q13.3	Kinase
33903_at	DAPK3	AB007144	5	Pass	13.00	5.61	9	Pass	TRUE	FALSE	5.22	2.49	death-associated protein kinase 3; DAPK3	19p13.3	Kinase
1134_at	ACK	L13738	6	Pass	25.00	7.07	12	Pass	TRUE	FALSE	10.00	2.50	activated p21cdc42Hs kinase; ACK1	3	Kinase
33223_at	KIAA0561	AB011133	6	Pass	16.17	7.17	13	Pass	TRUE	FALSE	6.46	2.50	KIAA0561 protein; KIAA0561		Kinase
32004_s_at	UNK_W32	W32483	6	Pass	10.83	5.04	13	Pass	TRUE	FALSE	4.31	2.51			Kinase
34679_at	BCR	X02596	5	Pass	17.00	2.00	12	Pass	TRUE	FALSE	6.67	2.55	breakpoint cluster region; BCR	22q11.23	Kinase
35365_at	ILK	U40282	6	Pass	30.17	5.98	13	Pass	TRUE	FALSE	11.62	2.60	integrin-linked kinase; ILK	11p15.5-p15.4	Kinase

Affy Qualifier	Affy Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of abs dec	7 of 13 present	Present in RA and Normal	Present in RA, Absent in Normal	Absent in RA, Present in Normal	Avg Freq (Normal)	Change RA / Normal	Name	Chromosome	Kinase or Phosphatase
38269_at	DKFZP386AL050147		6	Pass	44.67	9.63	13	Pass	TRUE	FALSE	FALSE	16.92	2.64	DKFZP386E0820 protein; 19	19	Kinase
1768_s_at	CSK	X59932	6	Pass	75.50	29.19	13	Pass	TRUE	FALSE	FALSE	27.77	2.72	c-src tyrosine kinase; CSK	15q23-q25	Kinase
38003_s_at	DGKZ	U94905	6	Pass	29.17	12.50	13	Pass	TRUE	FALSE	FALSE	10.23	2.85	diacylglycerol kinase, zeta (104kD); DGKZ		Kinase
138_at	MAP4K1	U66464	6	Pass	16.33	4.13	13	Pass	TRUE	FALSE	FALSE	5.69	2.87	mitogen-activated protein kinase kinase kinase 1; MAP4K1	19q13.1-q13.4	Kinase
993_at	TYK2	X54637	6	Pass	15.50	5.24	12	Pass	TRUE	FALSE	FALSE	5.25	2.95	tyrosine kinase 2; TYK2	19p13.2	Kinase
40215_at	ACK	L13738	6	Pass	13.33	5.05	10	Pass	TRUE	FALSE	FALSE	3.70	3.60	activated p21cdc42Hs kinase; ACK1		Kinase

Phosphatases

37384_at	KIAA0015	D13640	6	Pass	18.00	5.40	10	Pass	TRUE	FALSE	FALSE	8.80	2.05	KIAA0015 gene product; KIAA0015	22q11.22	Phosphatase
172_at	INPP5D	U57650	6	Pass	33.00	10.08	13	Pass	TRUE	FALSE	FALSE	16.08	2.05	inositol polyphosphate-5-phosphatase; I45KD; INPP5D	2q36-q37	Phosphatase
41162_at	PPM1G	Y13936	6	Pass	20.00	4.05	13	Pass	TRUE	FALSE	FALSE	9.23	2.17	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform; PPM1G		Phosphatase
382_at	PPP4C	X70218	6	Pass	16.83	7.36	13	Pass	TRUE	FALSE	FALSE	7.46	2.26	protein phosphatase 4 (formerly X), catalytic subunit; PPP4C	16p12-16p11	Phosphatase
210_at	PLCB2	M95678	6	Pass	49.17	20.53	12	Pass	TRUE	FALSE	FALSE	20.58	2.39	phospholipase C, beta 2; PLCB2	15q15	Phosphatase
41225_at	UNK_AL0	AL049417	6	Pass	9.17	4.88	13	Pass	TRUE	FALSE	FALSE	3.77	2.43	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related); DUSP3	17q21	Phosphatase
794_at	PTPN6	X62055	6	Pass	28.50	11.93	13	Pass	TRUE	FALSE	FALSE	10.69	2.67	protein tyrosine phosphatase, non-receptor type 6; PTPN6	12p13	Phosphatase
1005_at	DUSP1	X68277	6	Pass	21.17	21.76	13	Pass	TRUE	FALSE	FALSE	6.46	3.28	dual specificity phosphatase 1; DUSP1	5q34	Phosphatase

37864_s_at	IGHG3	Y14737	6	Pass	93.83	76.26	13	Pass	TRUE	FALSE	FALSE	8.00	11.73	immunoglobulin heavy constant gamma 3 (G3m marker); IGHG3	14q32.33	
36482_s_at	ATP2A3	Y15724	6	Pass	17.00	5.33	12	Pass	TRUE	FALSE	FALSE	3.25	5.23	ATPase, Ca++ transporting, ubiquitous; ATP2A3	17p13.3	
40644_g_at	ITGA2B	M34480	6	Pass	37.83	9.95	11	Pass	TRUE	FALSE	FALSE	7.45	5.08	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41B); ITGA2B	17q21.32	
32749_s_at	FLNA	AL050396	6	Pass	209.83	58.51	13	Pass	TRUE	FALSE	FALSE	41.46	5.06	filamin A, alpha (actin-binding protein-280); FLNA	Xq28	
33501_r_at	IGHA1	S71043	6	Pass	138.50	88.39	13	Pass	TRUE	FALSE	FALSE	28.92	4.79	immunoglobulin heavy constant alpha 1; IGH A1	14q32.33	
33822_at	NUNM1	Z11584	6	Pass	11.50	6.35	12	Pass	TRUE	FALSE	FALSE	2.42	4.76	nuclear mitotic apparatus protein 1; NUNM1	11q13	
38487_at	KIAA0246	D87433	6	Pass	35.50	24.04	8	Pass	TRUE	FALSE	FALSE	7.63	4.66	Stabilin-1		
1268_at	UBE1	M58028	6	Pass	47.50	14.10	13	Pass	TRUE	FALSE	FALSE	10.54	4.51	ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity immunoglobulin heavy constant delta; IGHD	Xp11.23	
37467_at	IGHD	K02882	6	Pass	25.17	37.82	10	Pass	TRUE	FALSE	FALSE	5.60	4.49	immunoglobulin heavy constant delta; IGHD	14q32.33	

Atty Qualifier	Atty Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of 7 of 13 present	Present in RA and Normal	Present in RA, Absent in Normal	Absent in RA, Present in Normal	Avg Freq (Normal)	Fold Change RA / Normal	Name	Chromosome	Kinase or Phosphatase
32378_at	PKM2	M26252	6	Pass	96.17	29.53	13	Pass	TRUE	FALSE	21.77	4.42	pyruvate kinase, muscle; PKM2	15q22	
39049_at	NOTCH4	AJ243937	6	Pass	47.33	13.25	13	Pass	TRUE	FALSE	11.31	4.19	Notch (Drosophila) homolog 4; NOTCH4	6p21.3	
33499_s_at	IGHA1	AF067420	6	Pass	125.33	74.06	13	Pass	TRUE	FALSE	29.62	4.16	immunoglobulin heavy constant alpha 1; IGHAI	14q32.33	
36028_at	TCIRG1	U45285	6	Pass	33.17	17.12	13	Pass	TRUE	FALSE	8.00	4.15	T-cell, immune regulator 1; TCIRG1	11q13.4-q13.5	
32070_at	PTPRCAP	X97267	6	Pass	119.83	16.22	13	Pass	TRUE	FALSE	28.92	4.14	protein tyrosine phosphatase, receptor type, c polypeptide-associated protein; PTPRCAP	11q13.3	
32588_s_at	BRF2	X78992	6	Pass	105.50	33.35	13	Pass	TRUE	FALSE	25.62	4.12	bulky response factor 2 (EGF-response factor 2); BRF2		
37014_at	MX1	M33882	6	Pass	27.50	22.98	13	Pass	TRUE	FALSE	6.69	4.11	myxovirus (influenza) resistance 1, homolog of murine (interferon-murine) receptor (granulocyte); CSF3R	21q22.3	
32623_at	GABBR1	AJ225028	6	Pass	18.17	4.17	7	Pass	TRUE	FALSE	4.43	4.10	gamma-aminobutyric acid (GABA) B receptor, 1; GABBR1	6p21.3	
596_s_at	CSF3R	M59820	6	Pass	40.67	20.97	12	Pass	TRUE	FALSE	9.92	4.10	colony stimulating factor 3 (granulocyte); CSF3R	1p35-p34.3	
1915_s_at	FOS	V01512	6	Pass	63.50	46.86	13	Pass	TRUE	FALSE	15.54	4.09	v-fos FBJ murine osteosarcoma viral oncogene homolog; FOS	14q24.3	
36412_s_at	IRF7	U53831	6	Pass	17.00	10.66	12	Pass	TRUE	FALSE	4.17	4.08	interferon regulatory factor 7; IRF7		
36138_at	CAPN4	X04106	6	Pass	57.67	25.33	13	Pass	TRUE	FALSE	14.38	4.01	calpain, small polypeptide; CAPN4		
36879_at	ECGF1	M63193	6	Pass	89.00	78.82	12	Pass	TRUE	FALSE	22.33	3.99	endothelial cell growth factor 1 (platelet-derived); ECGF1	22q13.33	
1916_s_at	FOS	V01512	6	Pass	46.17	29.96	13	Pass	TRUE	FALSE	12.00	3.85	v-fos FBJ murine osteosarcoma viral oncogene homolog; FOS	14q24.3	
33273_f_at	IGL@	X57809	6	Pass	180.83	155.56	13	Pass	TRUE	FALSE	47.38	3.82	immunoglobulin lambda locus; IGL@	22q11.1-q11.2	
34874_at	NTE	AJ004832	6	Pass	23.00	12.44	12	Pass	TRUE	FALSE	6.08	3.78	neuropathy target esterase; NTE		
41827_f_at	UNK_A193	AF032613	6	Pass	58.67	49.98	13	Pass	TRUE	FALSE	15.69	3.74	SMA3; SMA3	5q13	
38647_at	COPE	AJ131182	6	Pass	44.83	17.38	13	Pass	TRUE	FALSE	12.00	3.74	coatomer protein complex, subunit epsilon; COPE		
40164_at	ARHGDI1A	X69550	6	Pass	42.17	14.66	13	Pass	TRUE	FALSE	11.31	3.73	Rho GDP dissociation inhibitor (GDI) alpha; ARHGDI1A	17q25.3	
33500_f_at	IGHA1	S71043	6	Pass	109.33	64.26	13	Pass	TRUE	FALSE	30.00	3.64	immunoglobulin heavy constant alpha 1; IGHAI	14q32.33	
40718_at	CTSW	AF013611	6	Pass	30.50	19.00	10	Pass	TRUE	FALSE	8.40	3.63	cathepsin W (lysosomal); CTSW	11q13.1	
33143_s_at	SLC16A3	U81800	6	Pass	43.83	23.80	13	Pass	TRUE	FALSE	12.15	3.61	solute carrier family 16 (monocarboxylic acid transporters), member 3; SLC16A3	22q12.3-q13.2	
239_at	CTSD	M63138	6	Pass	76.50	38.12	13	Pass	TRUE	FALSE	21.31	3.59	cathepsin D (lysosomal aspartyl protease); CTSD	11p15.5	
33816_at	UNK_A10	AF020267	6	Pass	17.33	8.45	12	Pass	TRUE	FALSE	4.92	3.53	myosin IXB; MYO9B	19p13.1	
33283_at	ARRB2	AF106941	6	Pass	84.00	41.95	13	Pass	TRUE	FALSE	24.00	3.50	arrestin, beta 2; ARRB2	12p13	
32750_f_at	FLNA	X53416	6	Pass	23.00	3.95	10	Pass	TRUE	FALSE	6.60	3.48	filamin A, alpha (actin-binding protein-280); FLNA	Xq28	

Affy Qualifier	Affy Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of abs dec	Present in RA and Normal	Present in RA, Absent in Normal	Avg Freq RA, Present in Normal	Fold Change RA / Normal	Name	Chromosome	Kinase or Phosphatase	
31874_at	GAR22	Y07846	6	Pass	15.67	5.82	12	Pass	TRUE	FALSE	4.50	3.48	GAS2-related on chromosome 22; GAR22	22q12.2	
39997_at	PFC	AF005664	6	Pass	57.00	28.64	13	Pass	TRUE	FALSE	16.69	3.41	prolactin P factor, complement; PFC	Xp11.3-p11.23	
41045_at	SECTM1	U77643	6	Pass	29.67	22.56	13	Pass	TRUE	FALSE	8.69	3.41	secreted and transmembrane 1; SECTM1	17q25	
34412_s_at	GP1BB	U59632	6	Pass	85.50	35.30	13	Pass	TRUE	FALSE	25.08	3.41	glycoprotein Ib (platelet); GP1BB	22q11.21	
33274_f_at	IGL@	M18645	6	Pass	162.50	133.56	13	Pass	TRUE	FALSE	48.15	3.37	beta polypeptide; GP1BB	22q11.1-q11.2	
35170_at	MAN2C1	AF044414	6	Pass	21.50	5.43	10	Pass	TRUE	FALSE	6.40	3.36	mannosidase, alpha, class 2C, member 1; MAN2C1	15q11-q13	
41168_at	TAPBP	AF029750	6	Pass	112.50	29.72	13	Pass	TRUE	FALSE	34.00	3.31	TAP binding protein (tapasin); TAPBP	6p21.3	
37192_at	EPB49	U28389	6	Pass	56.67	18.65	12	Pass	TRUE	FALSE	17.17	3.30	erythrocyte membrane protein band 4.9 (denatun); EPB49	8p21.1	
38138_at	S100A11	D38583	6	Pass	74.83	42.88	13	Pass	TRUE	FALSE	22.77	3.29	S100 calcium-binding protein A11 (calgizzarin); S100A11	1q21	
41446_f_at	RNAHP	H68340	6	Pass	25.67	13.92	13	Pass	TRUE	FALSE	7.85	3.27	RNA helicase-related protein; RNAHP	17	
40643_at	ITGA2B	M34480	6	Pass	101.33	18.45	13	Pass	TRUE	FALSE	31.00	3.27	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41B); ITGA2B	17q21.32	
37966_at	UNK_AA1	AA187563	6	Pass	10.17	3.43	8	Pass	TRUE	FALSE		3.25	CGI-56 protein; CGI-56	22q13.2-q13.33	
33425_at	TIF1B	X97548	6	Pass	30.67	7.53	13	Pass	TRUE	FALSE	9.46	3.24	KRAB-associated protein 1; TIF1B	5	
36493_at	LSP1	M33552	6	Pass	49.17	23.56	13	Pass	TRUE	FALSE	15.31	3.21	lymphocyte-specific protein 1; LSP1	11p15.5	
34223_at	CSF3R	M59818	6	Pass	34.33	16.75	13	Pass	TRUE	FALSE	10.69	3.21	colony stimulating factor 3 receptor (granulocyte); CSF3R	1p35-p34.3	
34780_at	PLXNB2	AB002313	6	Pass	43.67	21.77	13	Pass	TRUE	FALSE	13.62	3.21	plexin B2; PLXNB2	22q13.33	
39649_at	ARHGAP4	X78817	6	Pass	53.00	19.42	13	Pass	TRUE	FALSE	16.54	3.20	Rho GTPase activating protein 4; ARHGAP4	Xq28	
35786_at	KIAA0476	AB007945	6	Pass	28.33	9.29	13	Pass	TRUE	FALSE	8.85	3.20	KIAA0476 gene product; 1	1	
39424_at	TNFRSF14	U70321	6	Pass	26.50	9.81	13	Pass	TRUE	FALSE	8.31	3.19	tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator); TNFRSF14	1p36.3-p36.2	
1353_g_at	IL8RA	U11870	4	Pass	12.75	2.22	8	Pass	TRUE	FALSE	4.00	3.19	interleukin 8 receptor, alpha; IL8RA	2q35	
35292_at	D6S81E	Z37166	6	Pass	29.83	5.04	13	Pass	TRUE	FALSE	9.38	3.18	HLA-B associated transcript-1; D6S81E	6p21.3	
33438_at	WBP2	AL040981	6	Pass	59.50	19.79	13	Pass	TRUE	FALSE	18.77	3.17	WW domain binding protein 2; WBP2	17q25	
36372_at	HK3	U51333	6	Pass	53.83	35.92	12	Pass	TRUE	FALSE	17.00	3.17	hexokinase 3 (white cell); HK3	5q35.2	
39182_at	EMP3	U87947	6	Pass	155.83	50.34	13	Pass	TRUE	FALSE	49.23	3.17	epithelial membrane protein 3; EMP3	19q13.3	
36229_at	IL17R	U58917	4	Pass	12.25	8.10	8	Pass	TRUE	FALSE	3.88	3.16	interleukin 17 receptor; IL17R	22q11.1	
33371_s_at	RAB31	U59877	6	Pass	34.17	14.36	13	Pass	TRUE	FALSE	10.85	3.15	RAB31, member RAS oncogene family; RAB31	18p11.3	
40332_at	7-60	AF109134	6	Pass	35.33	18.54	9	Pass	TRUE	FALSE	11.22	3.15	2-60 protein; 22098	20q13.3	
810_at	ARHGFE1	U64105	6	Pass	27.83	5.49	13	Pass	TRUE	FALSE	8.85	3.15	Rho guanine nucleotide exchange factor (GEF) 1; ARHGFE1	19q13.13	



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36960_at	EDR2	U89278	6	Pass	13.17	7.83	13	Pass	TRUE	FALSE	4.23	3.11	early development regulator 2 (homolog of polyhormetic 2); EDR2	1	
36785_at	HSPB1	Z23090	6	Pass	22.67	9.07	13	Pass	TRUE	FALSE	7.31	3.10	heat shock 27kD protein 1; HSPB1	7q	
39082_at	ANXA6	Y00097	6	Pass	62.00	12.18	13	Pass	TRUE	FALSE	20.15	3.08	annexin A6; ANXA6	5q32-q34	
39400_at	KIAA1055	AB028978	6	Pass	11.33	4.27	13	Pass	TRUE	FALSE	3.69	3.07	KIAA1055 protein; KIAA1055	15	
41106_at	KCNN4	AF022797	5	Pass	10.20	5.36	9	Pass	TRUE	FALSE	3.33	3.06	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4; KCNN4	19q13.2	
39076_s_at	DRAP1	AB091040	6	Pass	25.17	8.33	13	Pass	TRUE	FALSE	8.23	3.06	DR1-associated protein 1 (negative cofactor 2 alpha); DRAP1	11	
39112_at	USF2	Y07661	6	Pass	15.00	4.43	13	Pass	TRUE	FALSE	4.92	3.05	upstream transcription factor 2, c-fos interacting; USF2	19q13	
38813_at	TSC2	X75621	6	Pass	9.67	2.16	10	Pass	TRUE	FALSE	3.20	3.02	tuberous sclerosis 2; TSC2	16p13.3	
34789_at	PI6	S69272	6	Pass	23.83	10.76	13	Pass	TRUE	FALSE	7.92	3.01	protease inhibitor 6 (placental thrombin inhibitor); PI6	6p25	
37145_at	GNLY	M85276	6	Pass	11.17	70.80	13	Pass	TRUE	FALSE	37.00	3.00	granulysin; GNLY	2p12-q11	
34707_at	CHD3	U91543	6	Pass	21.83	7.25	13	Pass	TRUE	FALSE	7.31	2.99	chromodomain helicase DNA binding protein 3; CHD3	17p13.1	
38069_at	CLCN7	Z67743	6	Pass	29.83	6.77	11	Pass	TRUE	FALSE	10.00	2.98	chloride channel 7; CLCN7	16p13	
38063_at	UNK_U00	U00952	6	Pass	28.17	12.42	13	Pass	TRUE	FALSE	9.46	2.98	KIAA0233 gene product; KIAA0233	16	
37281_at	KIAA0233	D87071	6	Pass	36.33	11.18	13	Pass	TRUE	FALSE	12.23	2.97	immunoglobulin kappa variable ID-8; IGKV1D-8	2p12	
38194_s_at	IGKV1D-8	M63438	6	Pass	142.17	69.87	13	Pass	TRUE	FALSE	47.92	2.97	KIAA0050 gene product; KIAA0050		
37411_at	KIAA0050	D30758	6	Pass	34.33	9.40	12	Pass	TRUE	FALSE	11.58	2.96	ubiquitin specific protease 20; USP20		
36473_at	USP20	AB023220	6	Pass	16.17	3.66	12	Pass	TRUE	FALSE	5.50	2.94	GDP dissociation inhibitor 1; GDI1		
36152_at	GDI1	X79353	6	Pass	47.83	11.89	13	Pass	TRUE	FALSE	16.31	2.93	immunoglobulin lambda locus; IGL@		
35530_f_at	IGL@	X92997	6	Pass	30.17	22.56	11	Pass	TRUE	FALSE	10.36	2.91	polymerase (RNA) II (DNA directed)	22q11.1-q11.2	
40791_at	POLR2A	X63564	6	Pass	23.50	10.37	13	Pass	TRUE	FALSE	8.08	2.91	polypeptide A (220kD); POLR2A	17p13.1	
41753_at	ACTN4	U48714	6	Pass	30.83	12.92	13	Pass	TRUE	FALSE	10.69	2.88	actinin, alpha 4; ACTN4		
33925_at	NRGN	X99076	6	Pass	220.17	53.81	13	Pass	TRUE	FALSE	76.77	2.87	neurogranin (protein kinase C substrate, RC3);	19q13	
39689_at	CST3	A1362017	6	Pass	65.50	33.53	13	Pass	TRUE	FALSE	22.85	2.87	cystatin C (amyloid angiopathy and cerebral hemorrhage); CST3	11q24	
1107_s_at	ISG15	M13755	6	Pass	39.67	28.62	13	Pass	TRUE	FALSE	13.85	2.86	interferon-stimulated protein, L5 kDa; ISG15	20p11.2	
336_at	TBXA2R	D38081	5	Pass	11.80	2.59	7	Pass	TRUE	FALSE	4.14	2.85	thrombosane A2 receptor; TBXA2R	1	
31315_at	UNK_D84	D84143	5	Pass	22.00	16.09	8	Pass	TRUE	FALSE	7.75	2.84	H1 histone family, member X; H1FX	19p13.3	
319_g_at	H1FX	D64142	6	Pass	86.17	25.13	13	Pass	TRUE	FALSE	30.46	2.83	protease inhibitor 1 (anti-elastase), alpha-1-antitrypsin; PI		
36781_at	PI	X01683	6	Pass	101.67	57.50	13	Pass	TRUE	FALSE	36.00	2.82		14q32.1	

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41138_at	MIC2	M16279	6	Pass	74.50	25.15	13	Pass	TRUE	FALSE	26.38	2.82	antigen identified by monoclonal antibodies Yp11.3	Xp22.32, Yp11.3
41198_at	GRN	AF055008	6	Pass	69.00	41.70	11	Pass	TRUE	FALSE	24.45	2.82	granulin; GRN	17
41294_at	UBE1L	L13852	6	Pass	22.83	3.92	10	Pass	TRUE	FALSE	8.10	2.82	ubiquitin-activating enzyme E1, like; UBE1L	3p21
38894_g_at	NCF4	AL008637	6	Pass	18.83	7.91	13	Pass	TRUE	FALSE	6.69	2.81	neutrophil cytosolic factor 4 (40kD); NCF4	22q13.1
40668_s_at	CD6	U34624	4	Pass	11.00	4.76	11	Pass	TRUE	FALSE	3.91	2.81	CD6 antigen; CD6	11q13
38671_at	KIAA0620	AB014520	6	Pass	11.00	10.24	11	Pass	TRUE	FALSE	3.91	2.81	KIAA0620 protein	11q13
38686_at	ATP6DV	X71490	6	Pass	31.17	16.81	11	Pass	TRUE	FALSE	11.09	2.81	Vacuolar proton-ATPase, subunit D; V-ATPase, subunit D; ATP6DV	
35132_at	MYO1E	X98411	6	Pass	94.33	40.45	13	Pass	TRUE	FALSE	33.62	2.81	myosin IE; MYO1E	
34405_at	USP5	U47927	6	Pass	14.00	2.68	10	Pass	TRUE	FALSE	5.00	2.80	ubiquitin specific protease 5 (isopeptidase T); USP5	12p13
40667_at	CD6	X60992	6	Pass	31.83	11.62	13	Pass	TRUE	FALSE	11.38	2.80	CD6 antigen; CD6	11q13
31610_at	DD96	U21049	6	Pass	21.67	9.00	12	Pass	TRUE	FALSE	7.75	2.80	epithelial protein up-regulated in carcinoma, membrane associated	
39177_f_at	PPP2R4	X73478	6	Pass	25.33	13.09	13	Pass	TRUE	FALSE	9.08	2.79	protein phosphatase 2A, regulatory subunit B (PR 55); PPP2R4	9q34
36902_at	ARHG	X61587	6	Pass	42.67	17.57	13	Pass	TRUE	FALSE	15.31	2.79	ras homolog gene family, member G (rho G); ARHG	11p15.5-15.4
37387_f_at	KDEL1	X55885	6	Pass	14.17	5.56	12	Pass	TRUE	FALSE	5.08	2.79	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor	19q13.3
33535_at	P2RX1	U45448	6	Pass	9.17	4.17	10	Pass	TRUE	FALSE	3.30	2.78	purinergic receptor P2X, ligand-gated ion channel, 1; P2RX1	17p
36940_at	TIAF1	D86970	6	Pass	5.83	1.83	10	Pass	TRUE	FALSE	2.10	2.78	TGFB1-induced anti-apoptotic factor 1; TIAF1	17
39770_at	KIAA0250	D87437	6	Pass	8.83	3.97	11	Pass	TRUE	FALSE	3.18	2.78	KIAA0250 gene product	
39119_g_at	NK4	AA631972	6	Pass	79.33	22.00	13	Pass	TRUE	FALSE	28.62	2.77	natural killer cell transcript 4; NK4	16p13.3
41850_s_at	DIPA	U63825	6	Pass	12.33	5.39	11	Pass	TRUE	FALSE	4.45	2.77	hepatitis delta antigen-interacting protein A;	11
36843_at	SIPA1	AB005666	6	Pass	12.83	5.67	11	Pass	TRUE	FALSE	4.64	2.77	signal-induced proliferation-associated	11q13.3
38584_at	IFT4	AF026939	6	Pass	14.33	12.68	11	Pass	TRUE	FALSE	5.18	2.77	interferon-induced protein with tetratricopeptide repeats 4; IFT4	10q24
40955_at	UNK_U79	U79287	5	Pass	7.60	2.70	8	Pass	TRUE	FALSE	2.75	2.76	prostate tumor over-expressed gene 1; PTOV1	
35653_at	GPS2	U28963	6	Pass	24.00	6.39	13	Pass	TRUE	FALSE	8.69	2.76	G protein pathway suppressor 2; GPS2	
181_g_at	UNK_S82	S82470	6	Pass	26.17	15.45	10	Pass	TRUE	FALSE	9.50	2.75	BB1-malignant cell expression-enhanced gene/tumor progression-enhanced gene (human, UM-UC-9 bladder carcinoma cell line)	
38445_at	ARHGEF1	Y09160	6	Pass	24.33	6.77	13	Pass	TRUE	FALSE	8.85	2.75	Rho guanine nucleotide exchange factor (GEF) 1; ARHGEF1	19q13.13
37992_g_at	ATP5D	A1436567	6	Pass	34.83	13.91	13	Pass	TRUE	FALSE	12.69	2.74	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit; ATP5D	

HuPBMc\_RA\_U95A-Kin-PhosP.xls

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36780_at	CLU	M25915	6	Pass	248.17	77.71	13	Pass	TRUE	FALSE	90.46	2.74	clusterin (complement lytic inhibitor, SP-40/40, sulfated glycoprotein 2, testosterone-repressed transactivase 2, prostaglandin synthase 2, adaptor-related protein complex 1, gamma 2 subunit; AP1G2)	8p21-p12	
38798_s_at	GZAD	A1741833	6	Pass	16.67	3.27	13	Pass	TRUE	FALSE	6.08	2.74	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7 (18kD, B18); NDUFB7		
33773_i_at	NDUFB7	AA527880	6	Pass	12.33	6.35	10	Pass	TRUE	FALSE	4.50	2.74	adaptor-related protein complex 1, gamma 2 subunit; AP1G2		
36979_at	SLC2A3	M20681	6	Pass	39.83	11.44	13	Pass	TRUE	FALSE	14.54	2.74	solute carrier family 2 (facilitated glucose transporter), member 3; SLC2A3	12p13.3	
38517_at	ISGF3G	M87503	5	Pass	43.20	12.15	13	Pass	TRUE	FALSE	15.77	2.74	interferon-stimulated transcription factor 3; gamma (48kD); ISGF3G	14q11.2	
41161_at	DAXX	AB015051	6	Pass	33.50	15.22	13	Pass	TRUE	FALSE	12.23	2.74	death-associated protein 6; DAXX	6p21.3	
37591_at	UCP2	U94592	6	Pass	61.00	19.28	13	Pass	TRUE	FALSE	22.31	2.73	uncoupling protein 2 (mitochondrial, proton carrier); UCP2	11q13	
38391_at	CAPG	M94345	6	Pass	37.00	18.49	13	Pass	TRUE	FALSE	13.54	2.73	capping protein (actin filament), gelsolin-like; CAPG	2cen-q24	
33855_at	GRB2	M96995	6	Pass	16.17	6.97	13	Pass	TRUE	FALSE	5.92	2.73	growth factor receptor-bound protein 2; GRB2	17q24-q25	
35606_at	SGSH	U30894	6	Pass	33.17	9.20	13	Pass	TRUE	FALSE	12.15	2.73	N-sulfoglucosaminyl sulfohydrolase (sulfamidase); SGSH	17q25.3	
33916_at	I-1	AB023192	6	Pass	23.00	9.14	9	Pass	TRUE	FALSE	8.44	2.72	imidazole receptor candidate 1-1	3p21.1	
37100_at	C17ORF1B	AJ008112	6	Pass	22.17	6.55	13	Pass	TRUE	FALSE	8.15	2.72	chromosome 17 open reading frame 1B; C17ORF1B	17q21	
36554_at	ASMTL	Y15521	6	Pass	14.67	7.84	7	Pass	TRUE	FALSE	5.43	2.70	acetylserotonin O-methyltransferase-like; ASMTL	Xp22.3, Yp11.3	
31870_at	CD37	X14046	6	Pass	138.67	42.00	13	Pass	TRUE	FALSE	51.38	2.70	CD37 antigen; CD37	19p13-q13.4	
41047_at	UNK_A188	A1885170	6	Pass	36.50	8.19	13	Pass	TRUE	FALSE	13.54	2.70	immediate early protein; ETR101	19	
36097_at	ETR101	M62831	6	Pass	105.00	35.94	13	Pass	TRUE	FALSE	39.00	2.69	transportin-SK; TRNSR	7	
35813_at	TRNSR	AA192159	6	Pass	15.17	8.38	11	Pass	TRUE	FALSE	5.64	2.69	meny-CyC binding domain protein 3; MBD3	19p13.3	
41160_at	UNK_ACO	AC005943	6	Pass	8.67	5.75	9	Pass	TRUE	FALSE	3.22	2.69	SHC (Src homology 2 domain-containing) transforming protein 1; SHC1	1q21	
38118_at	SHC1	U73377	6	Pass	26.17	10.82	13	Pass	TRUE	FALSE	9.77	2.68	solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1; SLC25A1	22q11.21	
38997_at	SLC25A1	X96924	6	Pass	10.17	8.04	10	Pass	TRUE	FALSE	3.80	2.68	interferon regulatory factor 3; IRF3	19q13.3-q13.4	
371_at	IRF3	Z56281	6	Pass	15.67	3.88	7	Pass	TRUE	FALSE	5.86	2.67	peptidylprolyl isomerase B 15q21-cyclodextrin B; PPIB	15q21-q22	
35823_at	PPIB	M61573	6	Pass	75.00	22.64	13	Pass	TRUE	FALSE	28.08	2.67	RNA binding protein; A1; rich element binding factor; SRN300	16p13.3	
32761_at	KIAA0324	AB002222	6	Pass	35.33	7.58	13	Pass	TRUE	FALSE	13.23	2.67			

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33908_at	CAPN1	X04366	6	Pass	36.50	21.92	13	Pass	TRUE	FALSE	2.66	calpain, large polypeptide 1; CAPN1	11q13	
38597_at	SLC11A1	D50402	4	Pass	9.50	4.12	7	Pass	TRUE	FALSE	2.66	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1; SLC11A1	2q35	
36675_at	PNP1	J03191	6	Pass	174.17	57.46	13	Pass	TRUE	FALSE	2.66	profilin 1; PPN1	17p13.3	
32836_at	ACPAT1	U56417	6	Pass	25.33	2.80	13	Pass	TRUE	FALSE	2.66	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha)	6p21.3	
38417_at	AMPD2	M91029	6	Pass	27.00	10.08	12	Pass	TRUE	FALSE	2.66	adenosine monophosphate deaminase 2 (isoform 1); AMPD2	1p13.3	
39061_at	BST2	D28137	6	Pass	59.33	33.66	13	Pass	TRUE	FALSE	2.65	bone marrow stromal cell antigen 2; BST2	19p13.2	
38442_at	MFAP2	U19718	4	Pass	16.25	1.71	7	Pass	TRUE	FALSE	2.65	microfibrillar-associated protein 2; MFAP2	1p36.1-p35	
35629_at	UNK_AL01	AL022238	6	Pass	23.00	12.21	11	Pass	TRUE	FALSE	2.64	ribonuclease, RNase A family, 2 (liver, eosinophil-q31 derived neurotoxin); RNASE2	14q24-	
36766_at	RNASE2	X55988	6	Pass	37.50	29.43	13	Pass	TRUE	FALSE	2.64	ribonuclease, RNase A family, 2 (liver, eosinophil-q31 derived neurotoxin); RNASE2	14q24-	
34670_at	MAN2B1	U60899	6	Pass	31.00	10.68	13	Pass	TRUE	FALSE	2.63	mannosidase, alpha, class 2B, member 1; MAN2B1	19p13.1	
41164_at	IGHM	X67301	6	Pass	134.17	51.81	13	Pass	TRUE	FALSE	2.63	immunoglobulin heavy constant mu, IGHM	14q32.33	
1692_at	TIMP1	D11139	6	Pass	51.50	23.10	13	Pass	TRUE	FALSE	2.63	tissue inhibitor of metalloproteinase 1 (cryptoid potentiating activity, collagenase inhibitor); TIMP1	Xp11.3-p11.23	
36661_s_at	CD14	X06882	6	Pass	156.17	111.56	13	Pass	TRUE	FALSE	2.62	CD14 antigen, CD14	5q31.1	
37386_at	KDEL1	X55885	6	Pass	38.50	24.19	13	Pass	TRUE	FALSE	2.62	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1; KDEL1	19q13.3	
39358_at	NCOR2	U37146	6	Pass	22.17	10.13	13	Pass	TRUE	FALSE	2.62	nuclear receptor co-repressor 2; NCOR2	12q24	
31431_at	FCGRT	U12255	6	Pass	32.83	18.49	13	Pass	TRUE	FALSE	2.62	Fe fragment of IgG, receptor, transporter, alpha; FCGRT	19q13.3	
40725_at	GOSR1	AF047438	6	Pass	9.67	4.27	13	Pass	TRUE	FALSE	2.62	golgi SNAP receptor complex member 1; GOSR1	17q11	
1754_at	DAXX	AF006041	6	Pass	14.83	4.92	12	Pass	TRUE	FALSE	2.62	death-associated protein 6; DAXX	6p21.3	
37179_at	NFE2	S77763	6	Pass	15.50	8.02	13	Pass	TRUE	FALSE	2.62	nuclear factor (erythroid-derived 2), 45kD; NFE2	12q13	
1067_at	FLT3LG	U03858	6	Pass	8.50	1.87	12	Pass	TRUE	FALSE	2.62	fms-related tyrosine kinase 3 ligand; FLT3LG	19q13.3	
38547_at	ITGAL	Y00796	6	Pass	29.33	7.63	13	Pass	TRUE	FALSE	2.61	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha L; ITGAL)	16p11.2	
38730_at	KIAA0864	AB020671	6	Pass	22.50	3.94	13	Pass	TRUE	FALSE	2.61	KIAA0864 protein, kinesin-like 5 (mitotic kinesin-like protein 1); KNSL5		
33841_at	EIF5	R48209	6	Pass	10.83	3.87	12	Pass	TRUE	FALSE	2.60	kinesin-like protein 1; KNSL5		

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503_at	POLR2L	U37690	5	Pass	41.60	10.53	13	TRUE	FALSE	16.00	2.60	polymerase (RNA) II (DNA directed) polypeptide L (7.6kD); POLR2L	11p15	
39030_at	PABPN1	AF026029	6	Pass	24.00	7.40	13	TRUE	FALSE	9.23	2.60	poly(A)-binding protein, nuclear 1; PABPN1	14q11.2-q13	
947_at	MCM7	D55716	6	Pass	11.17	4.22	10	TRUE	FALSE	4.30	2.60	minichromosome maintenance deficient (S. cerevisiae) 7; MCM7	7q21.3-q22.1	
33836_at	NPIP	AC002045	6	Pass	12.33	2.25	8	TRUE	FALSE	4.75	2.60	nuclear pore complex interacting protein; NPIP	16p13-p11	
39910_at	UNK_AAG	AA663800	6	Pass	10.17	2.64	13	TRUE	FALSE	3.92	2.59	hypothetical protein; LOC51257		
33091_at	UNK_ABQ	AB007915	6	Pass	11.00	6.72	12	TRUE	FALSE	4.25	2.59	KIAA0446 gene product; KIAA0446	1	
1131_at	MAP2K2	L11285	6	Pass	24.83	5.19	13	TRUE	FALSE	9.62	2.58	mitogen-activated protein kinase kinase 2; MAP2K2	7q32	
40448_at	ZFP36	M92843	6	Pass	43.83	24.09	13	TRUE	FALSE	17.00	2.58	zinc finger protein homologous to Zfp-36 in mouse; ZFP36	19q13.1	
39280_at	TNRC5	U80744	6	Pass	10.50	5.32	11	TRUE	FALSE	4.09	2.57	truncal repeat containing 5; TNRC5	1	
35674_at	PD12	AB023211	4	Pass	10.25	6.13	7	TRUE	FALSE	4.00	2.56	peptidyl arginine deiminase, type II; PD12		
198_g_at	NME3	U29656	6	Pass	22.83	6.65	13	TRUE	FALSE	8.92	2.56	non-metastatic cells 3; protein expressed in; NME3	16q13	
31812_at	GMFR	M24470	6	Pass	19.17	7.63	12	TRUE	FALSE	7.50	2.56	guanosine monophosphate reductase; GMFR	6p23	
40296_at	UNK_ALQ	AL023653	6	Pass	29.83	11.70	13	TRUE	FALSE	11.69	2.55	aminolevulinic, delta-synthase 2	Xp11.21	
37285_at	ALAS2	X60364	6	Pass	84.33	43.66	13	TRUE	FALSE	33.08	2.55	antennal; ALAS2 (sideroblastic/hypochromic anemia)		
36994_at	ATP6C	M62762	6	Pass	60.17	24.26	13	TRUE	FALSE	23.62	2.55	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD;	16p13.3	
34532_at	UNK_AF0	AF035318	6	Pass	16.67	6.74	11	TRUE	FALSE	6.55	2.55			
33251_at	KIAA0779	AB018322	6	Pass	6.50	1.76	9	TRUE	FALSE	2.56	2.54	KIAA0779 protein; KIAA0779		
33860_at	KIAA0462	AB007931	6	Pass	21.67	6.28	13	TRUE	FALSE	8.54	2.54	KIAA0462 protein; KIAA0462	1	
39437_at	UNK_Z78	Z78324	6	Pass	18.33	7.20	13	TRUE	FALSE	7.23	2.54	SH3 domain-containing protein 6511; LOC51165		
39601_at	RDA32	AF061836	6	Pass	26.50	6.77	13	TRUE	FALSE	10.46	2.53	Ras association (RalGDS/AF-6) domain family 1; RASSF1	3p21.3	
32773_at	HLA-DQA	AA868382	6	Pass	57.83	23.45	13	TRUE	FALSE	22.92	2.52	major histocompatibility complex, class II, DQ alpha 1; HLA-DQA1	6p21.3	
33398_at	KIAA0670	AB014570	6	Pass	29.67	13.52	9	TRUE	FALSE	11.78	2.52	KIAA0670 protein/actin; KIAA0670	14	
31622_f_at	MTIF	M10943	5	Pass	29.00	15.70	11	TRUE	FALSE	11.55	2.51	metallothionein 1F (functional); MTIF	16q13	
36678_at	TAGLN2	D21261	6	Pass	175.00	42.08	13	TRUE	FALSE	69.69	2.51	transgelin 2; TAGLN2	16q21-q25	
33659_at	CFL1	X95404	6	Pass	207.83	56.94	13	TRUE	FALSE	82.92	2.51	cofilin 1 (non-muscle); CFL1	11q13	
497_at	CLN3	U32680	6	Pass	18.00	5.80	11	TRUE	FALSE	7.18	2.51	ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spidmeyer-Vogt disease); CLN3	16p12.1	

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39704_at	HMGY	L17131	5	Pass	20.40	4.77	7	Pass	TRUE	FALSE	8.14	2.51	high-mobility group (nonhistone chromosomal) protein isoforms I and Y; HMGY	6p21	
31432_at	FCGRT	U12255	6	Pass	57.33	28.74	12	Pass	TRUE	FALSE	22.92	2.50	Fc fragment of IgG, receptor, transporter, alpha; FCGRT	19q13.3	
31935_at	UNK_U75	U75968	5	Pass	17.20	5.07	8	Pass	TRUE	FALSE	6.88	2.50	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S cerevisiae CHL1-like helix); DD11	12p11	
35965_at	HSPA6	X51757	6	Pass	14.17	8.91	9	Pass	TRUE	FALSE	5.67	2.50	heat shock 70kD protein 6 (HSP70B); HSPA6	1cen-qter	
40867_at	PPP2R1A	J02902	5	Pass	30.40	5.94	12	Pass	TRUE	FALSE	12.17	2.50	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform; PPP2R1A		
32824_at	CLN2	AF039704	6	Pass	37.83	17.23	13	Pass	TRUE	FALSE	15.15	2.50	ceroid-lipidosis, neuronal 2, late infantile (Jansky-Bielschowsky disease); CLN2	11p15	
40098_at	EHD1	AF001434	6	Pass	18.50	3.21	12	Pass	TRUE	FALSE	7.42	2.49	EH domain containing 1; EHD1	11q13	
879_at	MX2	M30818	6	Pass	16.50	9.14	13	Pass	TRUE	FALSE	6.62	2.49	myxovirus (influenza) resistance 2, homolog of murine MX2	21q22.3	
1790_at	CDK10	X78342	6	Pass	18.50	6.16	7	Pass	TRUE	FALSE	7.43	2.49	cyclin-dependent kinase (CDC2-like) 10; CDK10	16q24	
4111_at	IFTM2	X57351	6	Pass	51.67	27.91	13	Pass	TRUE	FALSE	20.77	2.49	interferon induced transmembrane protein 2 (I-3D); IFTM2		
915_at	IFT1	M24594	4	Pass	9.25	3.30	11	Pass	TRUE	FALSE	3.73	2.48	interferon-induced protein 56; IFT1	10q25-q26	
38361_at	RASGRP2	A168812	6	Pass	14.50	0.84	13	Pass	TRUE	FALSE	5.85	2.48	RAS guanyl releasing protein 2 (calcium and DAG-regulated); RASGRP2	11q13	
38631_at	TNFAIP2	M92357	6	Pass	43.83	20.08	13	Pass	TRUE	FALSE	17.69	2.48	tumor necrosis factor, alpha-induced protein 2; TNFAIP2	14q32	
33207_at	PRKRI	A1095508	6	Pass	9.17	4.54	10	Pass	TRUE	FALSE	3.70	2.48	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor; PRKRI	14q32	
31673_at	CMAR	X65784	6	Pass	20.00	5.93	13	Pass	TRUE	FALSE	8.08	2.48	cell matrix adhesion regulator, spastic paraplegia 7, paraplegin (pure and complicated autosomal recessive); CMAR	16q1.1q24.3	
40099_at	LFP40	AB014551	6	Pass	20.00	10.20	13	Pass	TRUE	FALSE	8.08	2.48	rho/rac guanine nucleotide exchange factor (GEF) 2; ARIEGEF2		
34206_at	KIAA0782	AB018325	6	Pass	20.17	8.66	13	Pass	TRUE	FALSE	8.15	2.47	KIAA0782 protein; KIAA0782		
329_at	NUMA1	Z11584	6	Pass	18.83	5.27	13	Pass	TRUE	FALSE	7.62	2.47	nuclear mitotic apparatus protein 1; NUMA1	11q13	
36447_at	FCN1	S80990	6	Pass	246.17	113.27	13	Pass	TRUE	FALSE	99.69	2.47	ficollin (collagen/fibrinogen domain-containing) 1; signal transducer and activator of transcription 6; interleukin-4 inducible; FCN1	9q34	
41222_at	STAT6	AF067575	6	Pass	55.83	30.42	13	Pass	TRUE	FALSE	22.62	2.47	STAT6	12q13	

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35094_t_at	LILRA3	AF025527	6	Pass	26.00	15.35	12	Pass	TRUE	FALSE	FALSE	10.58	2.46	leukocyte immunoglobulin like receptor, subfamily A (without TM domain), member 3; LILRA3	19q13.4
33453_at	ATP6S1	A1000326	6	Pass	51.00	12.95	13	Pass	TRUE	FALSE	FALSE	20.77	2.46	ATPase, H <sup>+</sup> -transporting, lysosomal (vacuolar proton pump), subunit 1; member 3; LILRA3	Xq28
41409_at	ICB-1	AF044896	6	Pass	44.67	23.90	13	Pass	TRUE	FALSE	FALSE	18.23	2.45	basement membrane-induced gene; ICB-1	
33887_at	HGS	D84064	6	Pass	16.83	3.66	8	Pass	TRUE	FALSE	FALSE	6.88	2.45	human growth factor-regulated tyrosine kinase substrate; HGS	17q25
36936_at	TSTA3	U58766	6	Pass	10.17	1.60	13	Pass	TRUE	FALSE	FALSE	4.15	2.45	tissue specific transplantation antigen P35B; TSTA3	8q24.3
117_at	HSPA6	X51757	5	Pass	10.40	4.22	8	Pass	TRUE	FALSE	FALSE	4.25	2.45	heat shock 70kD protein 6 (HSP70B); HSPA6	1cen-qter
32211_at	PSMD13	AB009398	6	Pass	10.83	7.28	7	Pass	TRUE	FALSE	FALSE	4.43	2.45	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13; PSMD13	11p15.5
41337_at	AES	AF072902	6	Pass	49.67	16.39	13	Pass	TRUE	FALSE	FALSE	20.31	2.45	amino-terminal enhancer of split; AES	19p13.3
33230_at	NMP200	AJ131186	6	Pass	14.67	4.03	12	Pass	TRUE	FALSE	FALSE	6.00	2.44	nuclear matrix protein NMP200 related to	11q12.2
39062_at	PPGB	AL008726	6	Pass	53.17	15.46	13	Pass	TRUE	FALSE	FALSE	21.77	2.44	splicing factor PP19; protective protein for beta-galactosidase	20q13.1
40609_at	UNK_AJ47	AH75497	6	Pass	10.50	3.45	10	Pass	TRUE	FALSE	FALSE	4.30	2.44	RAS guanyl releasing protein 2 (calcium and DAG-regulated);	11q13
38359_at	RASGRP2	Y12336	6	Pass	54.67	8.16	13	Pass	TRUE	FALSE	FALSE	22.46	2.43	RASGRP2	
35807_at	CYBA	M21186	6	Pass	218.67	86.22	13	Pass	TRUE	FALSE	FALSE	89.92	2.43	cytochrome b-245, alpha polypeptide; CYBA	16q24
40875_s_at	SNRP70	X06815	6	Pass	75.00	22.68	13	Pass	TRUE	FALSE	FALSE	30.85	2.43	small nuclear ribonucleoprotein 70kD polypeptide (RNP antigen); SNRP70	19q13.3
39711_at	PRKCSH	J03075	6	Pass	18.50	5.09	13	Pass	TRUE	FALSE	FALSE	7.62	2.43	protein kinase C substrate	19p13.1-p13.2
39832_at	LOC51593	AL096723	6	Pass	12.33	3.61	12	Pass	TRUE	FALSE	FALSE	5.08	2.43	arsenate resistance protein	7q21
40160_at	DKFZP584	AL080109	6	Pass	15.67	4.46	13	Pass	TRUE	FALSE	FALSE	6.46	2.42	DKFZP584P2220 protein; DKFZP584P2220	
39823_at	H326	U06631	5	Pass	20.40	5.32	12	Pass	TRUE	FALSE	FALSE	8.42	2.42	H326; H326	
37351_at	UP	X90858	6	Pass	21.00	11.92	12	Pass	TRUE	FALSE	FALSE	8.67	2.42	uridine phosphorylase; UP	7
35566_t_at	UNK_AFO	AF015128	6	Pass	30.00	20.82	13	Pass	TRUE	FALSE	FALSE	12.38	2.42	zinc finger protein 151 (pH2-67); ZNF151	1p36.2-p36.1
41532_at	ZNF151	Y09723	6	Pass	8.17	2.40	8	Pass	TRUE	FALSE	FALSE	3.38	2.42	KIAA0542 gene product; KIAA0542	22q12.2
36545_s_at	UNK_ABQ	AB011114	6	Pass	11.17	3.31	13	Pass	TRUE	FALSE	FALSE	4.62	2.42	phosphatidylinositol transfer protein, membrane associated; PTPNM	11q13
38297_at	PTPNM	X98654	6	Pass	53.00	15.01	13	Pass	TRUE	FALSE	FALSE	21.92	2.42	natural killer cell group 7 sequence; NKG7	19
37121_at	NKG7	S69115	6	Pass	95.67	55.68	13	Pass	TRUE	FALSE	FALSE	39.62	2.41	glucosylase, alpha; acid storage disease type 11); GAA	17q25.2-q25.3
31816_at	GAA	X55079	6	Pass	18.00	9.32	11	Pass	TRUE	FALSE	FALSE	7.45	2.41		

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38029_at	MDU1	U02939	6	Pass	19.67	5.92	13	Pass	TRUE	FALSE	FALSE	8.15	2.41	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2; SLC3A2	11q13	
32550_s_at	CEBPA	Y11525	6	Pass	27.00	10.02	10	Pass	TRUE	FALSE	FALSE	11.20	2.41	CCAAT/enhancer binding protein (C/EBP), alpha; CEBPA	19q13.1	
31613_at	UNK_AAR	AA806239	5	Pass	8.60	1.52	7	Pass	TRUE	FALSE	FALSE	3.57	2.41			
40127_at	PMX1	M95929	6	Pass	16.67	5.20	13	Pass	TRUE	FALSE	FALSE	6.92	2.41	paired mesoderm homeo box 1; PMX1	1q24	
32116_at	UNK_AB0	AB002405	6	Pass	38.50	8.89	13	Pass	TRUE	FALSE	FALSE	16.00	2.41	expressed in activated T/LAK lymphocytes; LAK 4P	17q25	
41258_at	KIAA0618	N26665	6	Pass	35.50	6.25	13	Pass	TRUE	FALSE	FALSE	14.77	2.40	KIAA0618 gene product; hypothetical protein FLJ10267; FLJ10267 KIAA0618		
558_at	KRT1	M98776	5	Pass	12.20	5.26	13	Pass	TRUE	FALSE	FALSE	5.08	2.40	keratin 1 (epidermolytic hyperkeratosis; KRT1)	12q11-q13	
40414_at	VARS2	X59303	6	Pass	20.33	4.46	13	Pass	TRUE	FALSE	FALSE	8.46	2.40	val-tRNA synthetase 2; VARS2	6p21.3	
950_at	TUBB	X79535	6	Pass	23.00	7.13	7	Pass	TRUE	FALSE	FALSE	9.57	2.40			
37040_at	KIAA0088	D42041	6	Pass	37.50	11.67	13	Pass	TRUE	FALSE	FALSE	15.62	2.40	KIAA0088 protein; KIAA0088		
36161_at	ADTB2	M34175	6	Pass	18.83	7.94	13	Pass	TRUE	FALSE	FALSE	7.85	2.40	adaptor-related protein complex 2, beta 1 subunit; q12	17q11.2	
626_s_at	IFI35	L78833	5	Pass	5.40	4.04	8	Pass	TRUE	FALSE	FALSE	2.25	2.40	interferon-induced protein 35; IFI35	17q21	
36314_at	FLT3LG	U04806	6	Pass	13.50	3.67	11	Pass	TRUE	FALSE	FALSE	5.64	2.40	lms-related tyrosine kinase 3 ligand; FLT3LG	19q13.3	
36030_at	DKFZP586	AL080214	6	Pass	21.00	6.13	13	Pass	TRUE	FALSE	FALSE	8.77	2.39	DKFZP5862223 protein; DKFZP586223		
33833_at	SPTAN1	J05243	6	Pass	13.17	2.64	10	Pass	TRUE	FALSE	FALSE	5.50	2.39	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin); SPTAN1	9q33-q34	
33813_at	TNFRSF11	A181532	6	Pass	167.50	76.07	13	Pass	TRUE	FALSE	FALSE	70.08	2.39	tumor necrosis factor receptor superfamily, member 1B; TNFRSF11	1p36.3-p36.2	
38483_at	HSAA0191	A001916	6	Pass	37.50	15.98	13	Pass	TRUE	FALSE	FALSE	15.69	2.39	hypothetical protein; HSA011916	17p13	
33412_at	LGALS1	A1535946	6	Pass	99.50	46.06	13	Pass	TRUE	FALSE	FALSE	41.77	2.38	lectin, galactoside-binding, soluble 1 (galectin 1); LGALS1	22q13.1	
34749_at	SLC31A2	U83461	5	Pass	18.40	8.65	11	Pass	TRUE	FALSE	FALSE	7.73	2.38	solute carrier family 31 (copper transporters), member 2; SLC31A2	9q31-q32	
32660_at	UNK_AB0	AB002340	6	Pass	16.67	4.23	10	Pass	TRUE	FALSE	FALSE	7.00	2.38	KIAA0342 gene product; KIAA0342		
905_at	GUK1	L76200	6	Pass	46.33	17.22	13	Pass	TRUE	FALSE	FALSE	19.46	2.38	guanylate kinase 1; GUK1	1q32-q41	
277_at	MCL1	L08246	6	Pass	115.17	44.97	13	Pass	TRUE	FALSE	FALSE	48.38	2.38	myeloid cell leukemia sequence 1 (BCL2-related); MCL1	1q21	
922_at	PPP2R1A	J02902	6	Pass	33.50	8.36	13	Pass	TRUE	FALSE	FALSE	14.08	2.38	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform; PPP2R1A	2p13	
34433_at	DOK1	AF035299	6	Pass	20.33	17.93	11	Pass	TRUE	FALSE	FALSE	8.55	2.38	docking protein 1, cdkD (downstream of tyrosine kinase 1); DOK1	17q11.2-q12	
1403_s_at	SCYA5	M21121	6	Pass	181.00	62.86	13	Pass	TRUE	FALSE	FALSE	76.15	2.38	small inducible cytokine A5; RANTES; SCYA5		



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37026_at	COPEB	AF001461	6	Pass	26.50	13.94	13	Pass	TRUE	FALSE	11.15	2.38	core promoter element binding protein; COPEB	10p15	
1997_s_at	BAX	U19599	6	Pass	11.83	5.04	11	Pass	TRUE	FALSE	5.00	2.37	BCL2-associated X protein; BAX	19q13.3-q13.4	
33866_at	TPM4	X05276	6	Pass	7.33	1.63	10	Pass	TRUE	FALSE	3.10	2.37	transmembrane protein 4; TPM4	19p13.1	
38051_at	MAL	X76220	6	Pass	31.83	15.48	13	Pass	TRUE	FALSE	13.46	2.36	mal. T-cell differentiation protein; MAL	2cen-q13	
1347_at	CDC25B	S78187	6	Pass	33.83	10.44	13	Pass	TRUE	FALSE	14.31	2.36	cell division cycle 25B; CDC25B	20p13	
36603_at	GCN1L1	D86973	6	Pass	14.00	2.61	13	Pass	TRUE	FALSE	5.92	2.36	GCN1 (general control of amino-acid synthesis 1, yeast-like 1; GCN1L1, hypothetical protein; DKFZP586O0223	12q24.2	
36058_at	DKFZP586	AL096741	6	Pass	14.33	2.42	13	Pass	TRUE	FALSE	6.08	2.36	hypothetical protein; DKFZP586O0223	22	
40196_at	HYA22	D88153	5	Pass	10.40	3.65	12	Pass	TRUE	FALSE	4.42	2.35	HYA22 protein; HYA22	3p21.3	
33361_at	GNGLG	AF052149	6	Pass	14.67	2.66	13	Pass	TRUE	FALSE	6.23	2.35	guanine nucleotide binding protein (G protein), gamma 3, linked	1q12-q13.5	
34491_at	OASL	AJ225089	6	Pass	7.33	5.39	8	Pass	TRUE	FALSE	3.13	2.35	2'-5'-oligoadenylate synthetase-like; OASL	12q24.2	
41165_s_at	IGHM	X67301	6	Pass	150.00	56.88	13	Pass	TRUE	FALSE	63.92	2.35	immunoglobulin heavy constant mu; IGHM	14q32.33	
31504_at	HDLBP	M64098	6	Pass	13.67	4.68	12	Pass	TRUE	FALSE	5.83	2.34	high density lipoprotein binding protein (vigin); HDLBP	2q37	
1237_at	IER3	S81914	5	Pass	10.40	5.32	9	Pass	TRUE	FALSE	4.44	2.34	immediate early response 3; IER3	6p21.3	
38117_at	SEC24C	D38555	6	Pass	15.67	3.44	10	Pass	TRUE	FALSE	6.70	2.34	SEC24 (S. cerevisiae) related gene family, member C; SEC24C	10	
38423_at	UNK_L38	L38935	6	Pass	36.50	12.47	13	Pass	TRUE	FALSE	15.62	2.34	major vault protein; MVP	16p13.1-p11.2	
38064_at	LRP	X79882	6	Pass	23.17	10.70	13	Pass	TRUE	FALSE	9.92	2.33	activating transcription factor 5; ATFS		
39158_at	ATFS	AB021663	6	Pass	7.00	3.58	10	Pass	TRUE	FALSE	3.00	2.33	KIAA0843 protein; KIAA0843		
39597_at	KIAA0843	AB020650	6	Pass	10.50	4.97	12	Pass	TRUE	FALSE	4.50	2.33	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily 4, member 2; SMARCD2	17q23-q24	
34695_at	GAL7	A1816724	6	Pass	30.67	18.23	13	Pass	TRUE	FALSE	13.15	2.33	chemokine (C-C motif) receptor 1; CCR1	3p21	
39994_at	CCR1	D10925	5	Pass	17.60	14.91	9	Pass	TRUE	FALSE	7.56	2.33	asialoglycoprotein receptor 17p		
37799_at	ASGR2	X55284	6	Pass	13.33	6.31	11	Pass	TRUE	FALSE	5.73	2.33	2; ASGR2		
496_s_at	IL11RA	U32324	6	Pass	9.67	3.20	13	Pass	TRUE	FALSE	4.15	2.33	interleukin 11 receptor, alpha; IL11RA	9p13	
849_g_at	UNK_U19	U19261	6	Pass	10.00	2.45	13	Pass	TRUE	FALSE	4.31	2.32	TNF receptor-associated factor 1; TRAF1	9q33-q34	
34691_f_at	ARPC4	AF006087	6	Pass	25.00	6.63	13	Pass	TRUE	FALSE	10.77	2.32	actin related protein 2/3 complex, subunit 4 (20 kDa); ARPC4		
35244_at	KIAA0460	AB007929	5	Pass	11.60	3.65	11	Pass	TRUE	FALSE	5.00	2.32	KIAA0460 protein; KIAA0460	1	
32336_at	ALDOA	X05236	6	Pass	129.33	37.93	13	Pass	TRUE	FALSE	55.77	2.32	aldolase A; Fructose-bisphosphate; ALDOA	16q22-q24	
33818_at	DGS52E	M33519	6	Pass	30.67	4.37	13	Pass	TRUE	FALSE	13.23	2.32	H1A-B associated transcript-3; DGS52E	9p21.3	
40885_s_at	UNK_N30	N30151	6	Pass	18.33	2.58	13	Pass	TRUE	FALSE	7.92	2.31	eukaryotic translation initiation factor 4B; EIF4B		
38893_at	NCF4	AL008637	6	Pass	55.17	27.67	13	Pass	TRUE	FALSE	23.85	2.31	neutrophil cytosolic factor 4 (40kD); NCF4	22q13.1	

Atty Qualifier	Atty Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of 7 of 13 abs present dec	Present in RA and Normal	Present in RA, Absent in Normal	Avg Freq RA (normal)	Fold Change RA / Normal	Name	Chromosome	Location or Phosphatase
40365_at	GNAI5	M63904	6	Pass	15.83	7.47	13	Pass	FALSE	6.85	2.31	guanine nucleotide binding protein (G protein), alpha 15 (Gq class); GNAI5	19p13.3	
39795_at	CLAPM1	D63475	6	Pass	80.00	25.55	13	Pass	FALSE	34.62	2.31	adaptor-related protein complex 2, mu 1 subunit; AP2M1	3q28	
38729_at	FKBP4	M88279	6	Pass	11.17	3.06	12	Pass	FALSE	4.83	2.31	FK506-binding protein 4 (59kD); FKBP4		
39385_at	ANPEP	M22324	6	Pass	16.50	5.75	7	Pass	FALSE	7.14	2.31	alanine aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal)	15q25-q26	
37298_at	GABARAP	AF044671	6	Pass	123.67	48.80	13	Pass	FALSE	53.54	2.31	GABA(A) receptor-associated protein; GABARAP	17	
2019_s at	ITGB7	M68892	6	Pass	13.50	6.35	13	Pass	FALSE	5.85	2.31	integrin, beta 7; ITGB7	12q13.13	
36035_at	GPAAL	AB002135	6	Pass	24.33	6.83	13	Pass	FALSE	10.54	2.31	glycophosphatidylinositol anchor attachment 1; GPAAL	8q24.3	
37796_at	UNK_AFO	AF053156	6	Pass	28.33	2.94	11	Pass	FALSE	12.27	2.31	leucine-rich neuronal protein; LRN	7q22	
32174_at	SLC9A3R	AF015926	6	Pass	29.83	5.27	13	Pass	FALSE	12.92	2.31	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1; SLC9A3R		
36322_at	FUT7	AB012668	4	Pass	10.00	3.46	9	Pass	FALSE	4.33	2.31	fucosyltransferase 7 (alpha 1,3) fucosyltransferase; FUT7		
38091_at	LGALS9	Z49107	6	Pass	60.00	23.87	13	Pass	FALSE	26.00	2.31	lectin, galactoside-binding, soluble, 9 (galactin 9); LGALS9		
33706_at	SART1	AB006198	6	Pass	19.50	4.72	13	Pass	FALSE	8.46	2.30	squamous cell carcinoma antigen recognised by T cells; SART1		
1919_at	VAV1	X16316	4	Pass	13.25	3.77	8	Pass	FALSE	5.75	2.30	vav-1 oncogene; VAV1	19p13.2	
39053_at	HRP3P	AF016370	6	Pass	6.33	1.63	8	Pass	FALSE	2.75	2.30	U46f6-associated RNA splicing factor; HRP3P	1q21.1	
880_at	FKBP1A	M34539	6	Pass	59.33	20.33	13	Pass	FALSE	25.77	2.30	FK506-binding protein 1A (128D); FKBP1A	20p13	
37947_at	KIAA0043	D26362	6	Pass	16.50	8.46	12	Pass	FALSE	7.17	2.30	KIAA0043 gene product; ORF: LOC51035		
37376_at	LOC51035	M68864	6	Pass	28.33	9.73	13	Pass	FALSE	12.31	2.30			
32218_at	UNK_AFO	AF034176	6	Pass	31.67	11.67	13	Pass	FALSE	13.72	2.30			
41460_at	SIP	AF080561	6	Pass	9.00	3.95	12	Pass	FALSE	3.92	2.30	SYT interacting protein; SIP		
35749_at	TADA3L	AF060933	6	Pass	44.00	13.48	13	Pass	FALSE	19.15	2.30	transcriptional adaptor 3 (ADA3, yeast homolog)-like (PCAF histone acetylase complex); TADA3L		
38710_at	UNK_ALO	AL096714	6	Pass	29.67	8.82	13	Pass	FALSE	12.92	2.30	hypothetical protein FLJ20113; FLJ20113		
41386_t at	KIAA0346	AB002344	6	Pass	16.83	5.60	12	Pass	FALSE	7.33	2.30	KIAA0346 protein; KIAA0346	17p13.1	
344_s at	CNP	D13146	5	Pass	22.60	8.20	13	Pass	FALSE	9.85	2.30			
36162_at	BSG	X64364	6	Pass	18.00	2.28	13	Pass	FALSE	7.85	2.29	basigin; BSG	19p13.3	
36937_s at	CLIM1	U90878	6	Pass	18.17	6.40	13	Pass	FALSE	7.92	2.29	carboxy terminal LIM domain protein 1; CLIM1	10qter	

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1158_g_at	CALM3	J04046	6	Pass	22.50	4.04	11	Pass	TRUE	FALSE	9.82	calmodulin 3 (phosphatase kinase, delta); CALM3	19q13.2-q13.3	
38976_at	CORO1A	D44497	6	Pass	230.67	59.84	13	Pass	TRUE	FALSE	100.77	coronin, actin-binding protein 1A; CORO1A		
39722_at	NCOR1	AF044209	6	Pass	17.17	8.80	10	Pass	TRUE	FALSE	7.50	nuclear receptor co-regulator 1; NCOR1	17p11.2	
32909_at	AQP5	U46569	6	Pass	11.67	3.50	10	Pass	TRUE	FALSE	5.10	aquaporin 5; AQP5	12q13	
932_i_at	ZNF91	L11672	6	Pass	19.17	9.22	13	Pass	TRUE	FALSE	8.38	zinc finger protein 91 (HPE7_HTF10F_ZNF91_p12)	19p13.1	
39908_at	PAF65A	AF069735	6	Pass	111.50	49.03	9	Pass	TRUE	FALSE	48.78	PCAF associated factor 65		
31638_at	NDUFS7	AC005329	6	Pass	20.00	8.15	8	Pass	TRUE	FALSE	8.75			
33137_at	LTBPA	Y13622	6	Pass	12.00	2.90	12	Pass	TRUE	FALSE	5.25	latent transforming growth factor beta binding protein 4; LTBPA	19q13.1-q13.2	
39343_at	HSU53209	AW026656	6	Pass	7.17	4.12	7	Pass	TRUE	FALSE	3.14	transferrin-2 alpha (hnu-2 alpha); HSU53209		
32370_at	GZMB	M57888	6	Pass	46.83	29.69	13	Pass	TRUE	FALSE	20.34	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1); GZMB	14q11.2	
816_g_at	DOK1	U70987	6	Pass	30.17	18.29	13	Pass	TRUE	FALSE	13.23	docking protein 1, 62kD (downstream of tyrosine kinase 1); DOK1	2p13	
32658_at	UNK_AL031228		6	Pass	10.33	2.25	13	Pass	TRUE	FALSE	4.54	bromodomain-containing	6p21.3	
36208_at	FSRG1	D42040	6	Pass	20.83	4.36	13	Pass	TRUE	FALSE	9.15	2; BRD2		
38998_g_at	SLC25A1	X96924	6	Pass	11.83	3.82	10	Pass	TRUE	FALSE	5.20	solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1; SLC25A1	22q11.21	
33146_at	MCL1	L08246	6	Pass	116.17	36.29	13	Pass	TRUE	FALSE	51.08	myeloid cell leukemia sequence 1 (BCL2-related); MCL1	1q21	
402_a_at	ICAM3	X69819	6	Pass	46.33	18.16	13	Pass	TRUE	FALSE	20.38	intercellular adhesion molecule 3; ICAM3	19p13.3-p13.2	
39971_at	LYL1	M22637	6	Pass	13.83	3.54	11	Pass	TRUE	FALSE	6.09	lymphoblastic leukemia derived sequence 1; LYL1	19p13.2	
32646_at	KIAA0449	AB007918	5	Pass	22.20	3.56	9	Pass	TRUE	FALSE	9.78	KIAA0449 protein; KIAA0449	1	
31901_at	KCNAB2	AF044253	6	Pass	28.50	8.12	9	Pass	TRUE	FALSE	12.56	potassium voltage-gated channel, shaker-related subfamily, beta member 2; KCNAB2	1p36.3	
40147_at	VAT1	U18009	6	Pass	14.83	5.74	13	Pass	TRUE	FALSE	6.54	membrane protein of cholinergic synaptic vesicles; VAT1	17q21	
40130_at	FSTL1	U06863	6	Pass	17.00	5.66	12	Pass	TRUE	FALSE	7.50	folliculin-like 1; FSTL1	7q21.2-q31.1	
151_s_at	UNK_V00	V00599	6	Pass	42.17	11.99	13	Pass	TRUE	FALSE	18.62	tubulin, beta polypeptide; TUBB	6p21.3	
766_at	LGALS9	AB006782	6	Pass	31.33	14.72	13	Pass	TRUE	FALSE	13.85	lectin, galactoside-binding, soluble 9 (galectin 9); LGALS9		
33863_at	ORP150	U65785	6	Pass	25.50	5.61	11	Pass	TRUE	FALSE	11.27	oxygen regulated protein (150kD); ORP150	11	
41728_at	KIAA0152	D63486	6	Pass	19.83	5.00	13	Pass	TRUE	FALSE	8.77	KIAA0152 gene product; KIAA0152	12	
37307_at	GNAI2	X04828	6	Pass	147.67	57.65	13	Pass	TRUE	FALSE	65.31	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2; GNAI2	3p21	

Affy Qualifier	Affy Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of 7 of 13 present	Present in RA and Normal	Present in RA, Absent in Normal	Absent in Present in Normal	Avg Freq RA, (Normal)	Fold Change RA / Normal	Name	Chromosome	Phosphate
33826_at	CIZ1	AL120500	6	Pass	21.83	3.97	12	Pass	TRUE	FALSE	9.67	2.26	Cip1-interacting zinc finger protein, CIZ1	9q34.1	
1795_g_at	CCND3	M92287	6	Pass	94.50	24.91	13	Pass	TRUE	FALSE	41.85	2.26	cyclin D3; CCND3	6p21	
38674_at	IGFBP6	AA115140	6	Pass	103.50	49.49	13	Pass	TRUE	FALSE	45.85	2.26	hypothetical protein FLJ10262; FLJ10262	9	
39423_at	SPOF	AJ000644	6	Pass	12.50	7.74	11	Pass	TRUE	FALSE	5.55	2.25	speckle-type POZ protein; SPOF		
39133_at	GCN5L1	A1525379	5	Pass	7.00	2.00	9	Pass	TRUE	FALSE	3.11	2.25	GCN5 (general control of amino-acid synthesis, yeast, homolog-like 1; GCN5L1)	12q13-q14	
34224_at	KIAA0954	AC004770	6	Pass	4.67	3.33	13	Pass	TRUE	FALSE	2.08	2.25	retinoid X receptor, alpha; RXRA	9q34.3	
32800_at	RXRA	U66306	6	Pass	56.33	25.13	13	Pass	TRUE	FALSE	25.08	2.25	retinoid X receptor, alpha; RXRA	9q34.3	
33232_at	CRIP1	AI017574	6	Pass	73.33	19.72	13	Pass	TRUE	FALSE	32.69	2.24	cysteine-rich protein 1 (functional); CRIP1	7q11.23	
33352_at	H2BFQ	X57985	6	Pass	29.67	10.27	13	Pass	TRUE	FALSE	13.23	2.24	H2B histone family, member Q; H2BFQ	1q21-q23	
38724_at	KIAA0515	AB011087	6	Pass	10.17	1.83	13	Pass	TRUE	FALSE	4.54	2.24	KIAA0515 protein; KIAA0515		
1505_at	TYMS	D00596	5	Pass	7.00	2.00	8	Pass	TRUE	FALSE	3.13	2.24	thymidylate synthetase; TYMS	18p11.32	
36984_at	HPR	X89214	5	Pass	7.00	2.83	8	Pass	TRUE	FALSE	3.13	2.24	hepatoglobulin hepatoglobulin-related protein; HPR	16q22.1	
35302_at	TAP	AJ132712	6	Pass	53.50	14.82	13	Pass	TRUE	FALSE	23.92	2.24	nuclear RNA export factor 1 (Mex67, yeast, homolog); NXF1		
36996_at	OS-9	U41635	6	Pass	66.00	19.85	13	Pass	TRUE	FALSE	29.54	2.23	amplified in osteosarcoma; OS-9	12q13	
38672_at	PPPR10	Y13247	6	Pass	22.83	7.78	13	Pass	TRUE	FALSE	10.23	2.23	protein phosphatase 1, regulatory subunit 10; PPPR10	6p21.3	
41189_at	TNFRSF12	Y09392	6	Pass	11.50	4.18	13	Pass	TRUE	FALSE	5.15	2.23	tumor necrosis factor receptor superfamily, member 12 (translocating chain-association membrane protein); TNFRSF12	1p36.2	
38432_at	ISG15	AA203213	6	Pass	16.50	13.82	10	Pass	TRUE	FALSE	7.40	2.23	interferon-stimulated protein, 15 kDa; ISG15	1	
38279_at	GNAZ	D90150	6	Pass	11.83	4.62	13	Pass	TRUE	FALSE	5.31	2.23	guanine nucleotide binding protein (G protein), alpha 2 polypeptide; GNAZ	22q11.22	
38585_at	HBC2	M91036	6	Pass	101.50	94.05	12	Pass	TRUE	FALSE	45.58	2.23	hemoglobin, gamma A; hemoglobin, gamma G; HBG1, HBC2	11p15.5	
38112_at	CSPG2	X15998	6	Pass	69.67	52.00	13	Pass	TRUE	FALSE	31.31	2.23	chondroitin sulfate proteoglycan 2 (versican); CSPG2	5q14.3	
1274_at	CDC34	L22005	6	Pass	10.17	3.25	7	Pass	TRUE	FALSE	4.57	2.22	cell division cycle 34; CDC34	19p13.3	
1643_at	MTA1	U35113	6	Pass	8.00	2.19	10	Pass	TRUE	FALSE	3.60	2.22	metastasis associated 1; MTA1		
243_at	MAP4	M64571	6	Pass	10.00	3.63	10	Pass	TRUE	FALSE	4.50	2.22	microtubule-associated protein 4; MAP4	3p21	
37246_at	ARF5	M57567	6	Pass	46.67	18.51	12	Pass	TRUE	FALSE	21.00	2.22	ADP-ribosylation factor 5; ARF5	7q31.3	
37959_at	KIAA0154	D63876	6	Pass	20.00	7.38	13	Pass	TRUE	FALSE	9.00	2.22	KIAA0154 protein; ADP-ribosylation factor binding protein GGA3; KIAA0154	17	
38663_at	BCRP1	A1033692	6	Pass	23.50	7.23	12	Pass	TRUE	FALSE	10.58	2.22	Breakpoint cluster region protein, uterine leiomyoma, 1; barrier to autometastasis factor; BCRP1	14q24.1	

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37844_at	UNK_A126	A1263885	6	Pass	20.67	8.87	13	Pass	TRUE	FALSE	FALSE	9.31	2.22	class I cytokine receptor; WSX-1	19p13.11
32607_at	BASP1	AF030656	6	Pass	36.33	21.37	13	Pass	TRUE	FALSE	FALSE	16.38	2.22	brain acid-soluble protein	5p14-15
33396_at	GSTP1	U12472	6	Pass	70.17	32.53	13	Pass	TRUE	FALSE	FALSE	31.69	2.21	glutathione S-transferase p1; GSTP1	11q13
39330_s at	ACTN1	M95178	6	Pass	15.83	5.12	13	Pass	TRUE	FALSE	FALSE	7.15	2.21	actinin, alpha 1; ACTN1	14q24
38703_at	UNK_AF0	AF005050	6	Pass	16.17	4.07	13	Pass	TRUE	FALSE	FALSE	7.31	2.21	aspartyl aminopeptidase; DNPEP	
40723_at	SIT	AJ010059	6	Pass	16.17	4.62	13	Pass	TRUE	FALSE	FALSE	7.31	2.21	SHP2 interacting transmembrane adaptor; SIT	
464_s at	IF135	U72882	6	Pass	16.17	8.98	13	Pass	TRUE	FALSE	FALSE	7.31	2.21	interferon-induced protein 135; IF135	17q21
32226_at	MAP4	M64571	6	Pass	12.67	4.72	11	Pass	TRUE	FALSE	FALSE	5.73	2.21	microtubule-associated protein 4; MAP4	3p21
868_at	TAF2H	U13991	6	Pass	33.33	7.76	13	Pass	TRUE	FALSE	FALSE	15.08	2.21	TATA box binding protein (TBP)-associated factor; RNA polymerase II, H; 30kD; TAF2H	11p15.3
38056_at	KIAA0195	D83779	6	Pass	17.33	4.55	13	Pass	TRUE	FALSE	FALSE	7.85	2.21	KIAA0195 gene product; 17	
37898_r at	TFF3	A1085964	4	Pass	37.00	14.72	8	Pass	TRUE	FALSE	FALSE	16.75	2.21	trefoil factor 3 (intestinal); TFF3	21q22.3
654_at	MXI1	L07648	6	Pass	14.17	7.36	12	Pass	TRUE	FALSE	FALSE	6.42	2.21	MAX-interacting protein 1; MXI1	10q24- q25
33602_at	EDG6	AJ000479	6	Pass	27.17	6.34	13	Pass	TRUE	FALSE	FALSE	12.31	2.21	endothelial differentiation; G-protein-coupled receptor 6; EDG6	19p13.3
39308_r at	UNK_X81	X81637	6	Pass	9.67	2.88	13	Pass	TRUE	FALSE	FALSE	4.38	2.20	clathrin, light polypeptide 1(Lcb); CLTB	4q2-q3
37904_s at	GNI1	X66436	6	Pass	6.17	1.33	10	Pass	TRUE	FALSE	FALSE	2.80	2.20	ras homolog gene family, member C; ARHC	1p21-p13
1395_at	ARHC	L25081	5	Pass	13.00	7.11	11	Pass	TRUE	FALSE	FALSE	5.91	2.20	glucose phosphate isomerase; GPI	19q13.1
39122_at	GPI	K03515	6	Pass	33.00	7.87	13	Pass	TRUE	FALSE	FALSE	15.00	2.20	metallothionein 1B (functional); MT1B	10q13
609_f at	MT1B	M13485	4	Pass	27.00	5.72	11	Pass	TRUE	FALSE	FALSE	12.27	2.20	ribosomal protein L23- like; RPL23L	11p15.5
34358_at	RPL23L	Z49254	6	Pass	22.67	6.38	13	Pass	TRUE	FALSE	FALSE	10.31	2.20	glutamate receptor, metabotropic 4; GRM4	6p21.3
35485_at	GRM4	X80818	5	Pass	53.40	13.24	7	Pass	TRUE	FALSE	FALSE	24.29	2.20	sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase); SMPD1	11p15.4- p15.1
32574_at	SMPD1	X59960	6	Pass	13.17	4.17	13	Pass	TRUE	FALSE	FALSE	6.00	2.19	synaptobinding protein 2; STXB2	19p13.3- p13.2
38259_at	STXB2	AB002559	6	Pass	12.50	4.32	10	Pass	TRUE	FALSE	FALSE	5.70	2.19	acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl- Coenzyme A thiolase); ACAA1	3p23-p22
36417_s at	UNK_AF0	AF035295	6	Pass	15.17	5.23	12	Pass	TRUE	FALSE	FALSE	6.92	2.19	hypothetical protein FLJ20386; FLJ20386	
35154_at	UNK_W68	W68046	6	Pass	52.33	10.75	8	Pass	TRUE	FALSE	FALSE	23.88	2.19	S100 calcium-binding protein A4 (calcium protein, calvassulin, metastasin, murine placental homolog); S100A4	1q21
38087_s at	S100A4	W72186	6	Pass	177.67	62.89	13	Pass	TRUE	FALSE	FALSE	81.08	2.19		

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1583_at	TNFRSF11	M32315	6	Pass	92.83	44.60	13	Pass	FALSE	42.38	2.19	tumor necrosis factor receptor superfamily, member 1B; TNFRSF1B	1p36.3-p36.2	
214_at	MSX1	M97676	5	Pass	10.40	4.51	8	Pass	FALSE	4.75	2.19	msx1 (Drosophila) homeobox homolog 1 (formerly homeo box 7); MSX1	4p16.3-p16.1	
38789_at	TKT	L12711	6	Pass	97.00	62.34	13	Pass	FALSE	44.31	2.19	transketolase (Wernicke-Korsakoff syndrome);	3p14.3	
40106_at	E1B-AP5	AJ007509	6	Pass	32.83	11.87	13	Pass	FALSE	15.00	2.19	E1B-55kDa-associated protein 5; E1B-AP5		
38831_f_at	UNK_AF0	AF053356	6	Pass	67.17	23.27	13	Pass	FALSE	30.69	2.19	guanine nucleotide binding protein (G protein), beta polypeptide 2; GNB2	7q21.3-q22.1	
1804_at	KLK3	X07730	6	Pass	6.33	1.51	10	Pass	FALSE	2.90	2.18	kallikrein 3, (prostate specific antigen); KLK3	19q13	
38735_at	KIAA0513	AB011085	6	Pass	24.33	8.55	13	Pass	FALSE	11.15	2.18	KIAA0513 gene product;		
41443_at	TTC	U63127	6	Pass	25.67	6.02	13	Pass	FALSE	11.77	2.18	SEC7 homolog, TTC	2q13	
38119_at	GYPC	X12496	6	Pass	56.33	19.66	13	Pass	FALSE	25.85	2.18	glycophorin C (Gerbich blood group); GYPC	2q14-q21	
39594_f_at	MT1H	R93327	6	Pass	28.67	10.27	13	Pass	FALSE	13.15	2.18	metallothionein 1H;	10q13	
41421_at	KIAA0909	AB020716	6	Pass	12.17	5.12	12	Pass	FALSE	5.58	2.18	KIAA0909 protein;		
40712_at	ADAM8	D26579	6	Pass	44.00	15.09	13	Pass	FALSE	20.23	2.17	a disintegrin and metalloprotease domain 8; ADAM8	10q26.3	
40569_at	ZNF42	M58297	6	Pass	8.33	1.51	12	Pass	FALSE	3.83	2.17	zinc finger protein 42 (myeloid-specific retinoid acid responsive); ZNF42	19q13.2-q13.4	
283_at	UQCRC1	L16842	6	Pass	27.17	10.46	12	Pass	FALSE	12.50	2.17	ubiquinol-cytochrome c reductase core protein 1; UQCRC1	3p21.3	
40100_at	LFP40	U72206	6	Pass	16.00	5.66	11	Pass	FALSE	7.36	2.17	thioreac guanine nucleotide exchange factor (GEF) 2; AREGEP2		
1878_at	ERCC1	M13194	6	Pass	14.33	4.50	10	Pass	FALSE	6.60	2.17	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence); ERCC1	19q13.2-q13.3	
37329_at	NDUFV1	AF053070	6	Pass	17.00	6.07	12	Pass	FALSE	7.83	2.17	NADH dehydrogenase (ubiquinone) flavoprotein 1 (51kD); NDUFV1	11q13	
41177_at	UNK_AW4	AW024285	6	Pass	35.33	17.08	13	Pass	FALSE	16.31	2.17	polymerase (RNA) II (DNA directed)		
41332_at	POLR2E	D38251	6	Pass	19.50	7.34	7	Pass	FALSE	9.00	2.17	polypeptide E (25kD); POLR2E	19p13.3	
1061_at	IL10RA	U00672	6	Pass	31.00	7.77	13	Pass	FALSE	14.31	2.17	interleukin 10 receptor, alpha; IL10RA	11q23	
32529_at	PG3	X69910	6	Pass	14.00	8.88	13	Pass	FALSE	6.46	2.17	transmembrane protein (63kD), endoplasmic reticulum/Golgi intermediate compartment; PG3	12	
32681_at	SLC9A1	S68616	6	Pass	24.67	6.77	13	Pass	FALSE	11.38	2.17	solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (anionporter, Na+/H+, amiloride sensitive); SLC9A1	1p36.1-p35	

HuPBMc\_RA\_U95A-Kin-PhosP.xls

Atfy Qualifier	Atfy Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of abs dec	7 of 13 present	Present In RA and Normal	Present In RA, Absent In Normal	Absent In RA, Present In Normal	Avg Freq (Normal) RA / Normal	Fold Change RA / Normal	Name	Chromosome	Phosphatase
38354_at	CEBPB	X42560	6	Pass	74.00	37.56	13	Pass	TRUE	FALSE	FALSE	34.15	2.17	CCAAT/enhancer binding protein (CEBP), beta; CEBPB	20q13.1	
38397_at	UNK_U09	U09196	6	Pass	19.33	5.24	13	Pass	TRUE	FALSE	FALSE	8.92	2.17			
39339_at	KIAA0792	AB018335	6	Pass	20.83	5.19	13	Pass	TRUE	FALSE	FALSE	9.62	2.17	KIAA0792 gene product; KIAA0792		
41084_at	UNK_A165	AF659108	6	Pass	12.50	3.62	13	Pass	TRUE	FALSE	FALSE	5.77	2.17			
35826_at	SUP35H	AF040253	6	Pass	16.83	5.08	9	Pass	TRUE	FALSE	FALSE	7.78	2.16	suppressor of Ty (S.cerevisiae) 5 homolog; SUP35H	19q13	
34231_at	UNK_AFO	AF074606	6	Pass	17.50	6.86	11	Pass	TRUE	FALSE	FALSE	8.09	2.16	histone acetyltransferase; HBOA	Xq21	
33261_at	HLA-DRB	M16941	6	Pass	146.83	54.47	13	Pass	TRUE	FALSE	FALSE	67.92	2.16	major histocompatibility complex, class II, DR beta chain; HLA-DRB1	6p21.3	
33213_at	RRBP1	AF006751	6	Pass	8.83	5.12	11	Pass	TRUE	FALSE	FALSE	4.09	2.16	ribosome binding protein 1 (dog, 180kD homolog); RBBP1	20p12	
37148_at	LILRB3	AF025533	6	Pass	44.50	25.98	13	Pass	TRUE	FALSE	FALSE	20.62	2.16	leukocyte immunoglobulin like receptor, subfamily B (with TM and ITIM domains), member 3; LILRB3	19q13.4	
35336_at	KIAA0688	AL021707	6	Pass	105.00	25.46	13	Pass	TRUE	FALSE	FALSE	48.77	2.15	CDC37 (cell division cycle 37, S. cerevisiae); homolog; CDC37	19	
505_at	CDC37	U43077	6	Pass	48.50	9.75	13	Pass	TRUE	FALSE	FALSE	22.54	2.15			
37706_at	GLG1	U28811	6	Pass	14.67	2.50	11	Pass	TRUE	FALSE	FALSE	6.82	2.15	Golgi apparatus protein 1; GLG1	16q22-q23	
37650_at	UNK_U41	U41315	6	Pass	43.33	11.57	13	Pass	TRUE	FALSE	FALSE	20.15	2.15	makorin, ring finger protein, L; MKRN1	7q34	
33360_at	KIAA1004	AB023221	6	Pass	20.33	3.01	13	Pass	TRUE	FALSE	FALSE	9.46	2.15	box and leucine-rich repeat protein 1; FBXL11		
36933_at	NDRG1	D87953	6	Pass	19.67	6.25	13	Pass	TRUE	FALSE	FALSE	9.15	2.15	N-myc downstream regulated; NDRG1	8	
33824_at	KRT8	X74929	6	Pass	24.17	8.61	12	Pass	TRUE	FALSE	FALSE	11.25	2.15	CGI-39 protein, keratin 8; KRT8, LOC51079	12q13	
36634_at	BTG2	U72649	6	Pass	38.67	16.39	13	Pass	TRUE	FALSE	FALSE	18.00	2.15	BTG family, member 2; BTG2	1q22	
38641_at	UNK_A11	AJ131315	6	Pass	15.83	4.75	8	Pass	TRUE	FALSE	FALSE	7.38	2.15	IMP (inosine monophosphate) dehydrogenase 1; subunit; AP2S1	7q21.3-q22	
40695_at	IMPDH1	J05272	6	Pass	35.67	14.80	13	Pass	TRUE	FALSE	FALSE	16.62	2.15			
39347_at	CLAPS2	X97074	6	Pass	50.67	17.93	13	Pass	TRUE	FALSE	FALSE	23.62	2.15	adaptor-related protein complex 2, sigma 1 subunit; AP2S1	19q13.2-q13.3	
39134_at	TON1	AJ006973	6	Pass	7.50	2.66	10	Pass	TRUE	FALSE	FALSE	3.50	2.14	target of myb1 (chicken) homolog; TON1	22q13.1	
35770_at	ATP6S1	D16469	6	Pass	44.00	20.62	13	Pass	TRUE	FALSE	FALSE	20.54	2.14	ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump), subunit 1; metallothionein 1E (functional); MT1E	Xq28	
36130_f_at	MT1E	R02331	6	Pass	25.67	6.95	12	Pass	TRUE	FALSE	FALSE	12.00	2.14		16q13	
506_g_at	STAT5A	U43185	6	Pass	22.83	4.88	13	Pass	TRUE	FALSE	FALSE	11.15	2.14	signal transducer and activator of transcription 5A; STAT5A	17q11.2	
32192_g_at	ZNF144	D13969	6	Pass	18.00	4.20	7	Pass	TRUE	FALSE	FALSE	8.43	2.14	zinc finger protein 144 (Med-18); ZNF144	17	
32197_at	SLC25A11	AF070548	6	Pass	11.17	4.31	13	Pass	TRUE	FALSE	FALSE	5.23	2.13	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11; SLC25A11	17p13.3	
40980_at	UNK_W28	W26477	6	Pass	11.17	2.93	13	Pass	TRUE	FALSE	FALSE	5.23	2.13			

Ally Qualifier	Ally Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of abs dec	Present in RA and Normal	Present in RA, Absent in Normal	Avg Freq RA (Normal)	Fold Change RA / Normal	Name of Gene	Chromosome	Refseq or Phosphatase
32717_at	NEURL	AF029729	4	Pass	27.75	5.74	8	TRUE	FALSE	13.00	2.13	neutralized (Drosophila)-like; NEURL	10q25.1	
38700_at	CSRP1	M3146	6	Pass	11.83	3.66	11	TRUE	FALSE	5.55	2.13	cysteine and glycine-rich protein 1; CSRP1	1q32	
38718_at	DKFZP386AL050101		6	Pass	8.00	2.10	12	TRUE	FALSE	3.75	2.13	DKFZP386E1519 protein; DKFZP386E1519		
33390_at	UNK_AA2	AA203487	6	Pass	83.67	49.40	9	TRUE	FALSE	39.22	2.13	DKFZP386E1519		
829_s_at	GSTP1	U21689	6	Pass	51.83	30.04	10	TRUE	FALSE	24.30	2.13	glutathione S-transferase pi; GSTP1	11q13	
39778_at	MGAT1	M55621	6	Pass	39.67	12.47	13	TRUE	FALSE	18.62	2.13	mammalian (alpha-1,3)-glycosyltransferase; MGAT1	5q35	
40153_at	ABCB2	X57522	6	Pass	29.50	8.67	13	TRUE	FALSE	13.85	2.13	ATP-binding cassette, subfamily B (MDR/TAP), member 2; ABCB2	6p21.3	
404_at	IL4R	X52425	6	Pass	29.00	8.29	13	TRUE	FALSE	13.62	2.13	interleukin 4 receptor; IL4R	16p11.2-12.1	
37101_at	DKFZP364AL050008		6	Pass	19.17	5.19	12	TRUE	FALSE	9.00	2.13	DKFZP364A063 protein; DKFZP364A063		
32904_at	PRF1	M28393	6	Pass	86.00	65.71	13	TRUE	FALSE	40.38	2.13	perforin 1 (preforming protein); PRF1	10q22	
33228_s_at	IL10RB	AI984234	6	Pass	55.50	17.95	13	TRUE	FALSE	26.08	2.13	interleukin 10 receptor, beta; IL10RB	21q22.11	
40421_at	PIN1	U49070	6	Pass	8.67	2.58	12	TRUE	FALSE	4.08	2.12	protein (peptidyl-prolyl isomerase) NIMA interacting 1; PIN1	19p13	
691_g_at	P4HB	J02783	6	Pass	49.17	17.06	12	TRUE	FALSE	23.17	2.12	procollagen-proline, 2-oxoglutarate 4-hydroxylase; beta polypeptide (protein disulfide isomerase; inter-alpha-trypsin inhibitor heavy chain subunit 1); PIN1	17q25	
1363_s_at	TNFRSF1A	M58286	6	Pass	28.17	11.91	11	TRUE	FALSE	13.27	2.12	tumor necrosis factor receptor superfamily, member 1A; TNFRSF1A	12p13.2	
330_s_at	TUBA1	X06956	6	Pass	39.17	9.47	13	TRUE	FALSE	18.46	2.12	tubulin, alpha 1 (testis specific); TUBA1	2q	
41622_s_at	ZNF266	AA868898	6	Pass	6.83	1.83	9	TRUE	FALSE	3.22	2.12	zinc finger protein 266; ZNF266		
286_at	H2AFO	L19779	6	Pass	61.50	25.26	13	TRUE	FALSE	29.00	2.12	H2A histone family, member O; H2AFO		
41282_s_at	PEX10	AA194159	4	Pass	11.50	3.70	7	TRUE	FALSE	5.43	2.12	peroxisome biogenesis factor 10; PEX10		
41745_at	IFTM3	X57352	6	Pass	207.17	120.90	13	TRUE	FALSE	97.85	2.12	interferon induced transmembrane protein 3 (IL8U); IFTM3		
31845_at	ELF4	U32645	6	Pass	18.17	7.70	12	TRUE	FALSE	8.58	2.12	E74-like factor 4 (cis domain transcription factor); ELF4	Xq26	
1116_at	CD19	M28170	6	Pass	6.83	1.33	13	TRUE	FALSE	3.23	2.12	CD19 antigen; CD19	16p11.2	
40688_at	LAT	AJ223280	6	Pass	27.67	4.37	12	TRUE	FALSE	13.08	2.11	linker for activation of T cells; LAT		
162_at	USP11	U44839	6	Pass	46.17	9.66	13	TRUE	FALSE	21.83	2.11	ubiquitin specific protease 11; USP11	Xp21.2-p11.2	
34906_g_at	UNK_AA3	AA97136	6	Pass	32.50	8.85	13	TRUE	FALSE	15.38	2.11	docking protein 2, 5kD; DOK2		
31514_at	DOK2	AF034970	6	Pass	25.33	8.80	10	TRUE	FALSE	12.00	2.11			
37002_at	BLVRB	D32143	6	Pass	25.00	11.47	13	TRUE	FALSE	11.85	2.11	biliverdin reductase B (flavin reductase (NADPH)); BLVRB	19q13.1-q13.2	
1357_at	USP4	U20657	6	Pass	12.33	4.59	13	TRUE	FALSE	5.85	2.11	ubiquitin specific protease 4 (proto-oncogene); USP4	3p21.3	



Affy Qualifier	Affy Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of abs dec	7 of 13 present	Present in RA and Normal	Present in RA, Absent in Normal	Absent in RA, Present in Normal	Avg Freq (Normal)	Fold Change RA / Normal	Name	one	Knase or Phosphatase
323172_at	SULT1A2	U34804	6	Pass	24.50	11.33	13	Pass	TRUE	FALSE	FALSE	11.62	2.11	sulfotransferase family 1A, phenol-preferring, member 1; 2.sulfotransferase family 1A, phenol-preferring, member 1;	16p12.1-2	
32774_at	NDUFB7	AA327880	6	Pass	24.33	7.55	13	Pass	TRUE	FALSE	FALSE	11.54	2.11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7 (18kD, B18), NDUFB7	3p21.3	
40870_g_at	RBM6	AF060517	6	Pass	12.17	3.97	13	Pass	TRUE	FALSE	FALSE	5.77	2.11	RNA binding motif protein 6; RBM6	16q13	
39081_at	MT2A	AI547258	6	Pass	11.83	4.31	13	Pass	TRUE	FALSE	FALSE	5.62	2.11	metallothionein 2A; metallothionein 2;	17q25	
1375_g_at	TIMP2	M32304	4	Pass	14.75	8.26	9	Pass	TRUE	FALSE	FALSE	7.00	2.11	issue inhibitor of metalloproteinase 2; TIMP2	3p21.1	
36615_at	ARP	M81751	4	Pass	19.25	5.50	8	Pass	TRUE	FALSE	FALSE	9.38	2.11	Arginine-rich protein; mitochonosome maintenance deficient (S. cerevisiae) 2 (mitotin); MCM2	3q21	
35312_at	MCM2	D21063	6	Pass	17.50	3.02	13	Pass	TRUE	FALSE	FALSE	8.31	2.11	Arginine-rich protein; mitochonosome maintenance deficient (S. cerevisiae) 2 (mitotin); MCM2	6p21.3	
37801_at	TJ6	AF112972	6	Pass	9.00	3.58	11	Pass	TRUE	FALSE	FALSE	4.27	2.11	TJ6 protein; TJ6		
38621_at	UNK_AJ0	AJ012008	6	Pass	10.00	2.45	12	Pass	TRUE	FALSE	FALSE	4.75	2.11	dimethylarginine dimethylaminohydrolase 2; DDAH2		
37939_at	UNK_AL0	AL022318	6	Pass	45.67	11.69	13	Pass	TRUE	FALSE	FALSE	21.69	2.11	small inducible cytokine	17q11.2-	
14051_at	SCYA5	M21121	6	Pass	68.17	25.93	13	Pass	TRUE	FALSE	FALSE	32.38	2.10	AS (RANTES); SCYA5	12	
35150_at	TNFRSF5	X60592	6	Pass	28.33	7.66	13	Pass	TRUE	FALSE	FALSE	13.46	2.10	tumor necrosis factor receptor superfamily, member 5; TNFRSF5	20q12-2	
34864_at	CGI-57	AF070638	6	Pass	38.17	12.35	13	Pass	TRUE	FALSE	FALSE	18.15	2.10	hypothetical protein; CGI-57		
34861_at	GOLGA3	D63997	6	Pass	10.83	1.47	13	Pass	TRUE	FALSE	FALSE	5.15	2.10	golgi autoantigen, poligin subunit 3; GOLGA3	12	
32253_at	ATN1L	AB007927	6	Pass	31.67	4.97	13	Pass	TRUE	FALSE	FALSE	15.08	2.10	arginine glutamic acid dipeptide RE repeats; RERE	1p36.1-	
41264_at	UNK_AL0	AL050172	4	Pass	6.00	2.94	7	Pass	TRUE	FALSE	FALSE	2.86	2.10	ubiquitin specific protease 15; USP15	12q14	
34295_at	USP15	AB011101	6	Pass	6.00	3.16	7	Pass	TRUE	FALSE	FALSE	2.86	2.10	ubiquitin specific protease 15; USP15	12q14	
40780_at	CTBP2	AF016507	6	Pass	15.33	10.46	13	Pass	TRUE	FALSE	FALSE	7.31	2.10	C-terminal binding protein 2; CTBP2	21q21.3	
38453_at	ICAM2	X15606	6	Pass	25.50	5.36	13	Pass	TRUE	FALSE	FALSE	12.15	2.10	intercellular adhesion molecule 2; ICAM2	17q23-	
36889_at	FCER1G	M33195	6	Pass	56.00	35.60	13	Pass	TRUE	FALSE	FALSE	26.69	2.10	Fe fragment of IgE, high affinity 1, receptor for; gamma polypeptide; FCER1G	1q23	
38053_s_at	BRE	AF015767	6	Pass	9.83	3.13	13	Pass	TRUE	FALSE	FALSE	4.69	2.10	brain and reproductive organ-expressed (TNFRSF1A modulator); BRE		
32816_at	SGT	AL050156	6	Pass	6.67	2.25	11	Pass	TRUE	FALSE	FALSE	3.18	2.10	small glutamine-rich tetrapeptide repeat (TPR)-containing; SGT	19p13	
36986_at	UNK_AL0	AL031295	6	Pass	117.17	29.18	13	Pass	TRUE	FALSE	FALSE	55.92	2.10	trypanophyl-RNA synthetase; WARS	14q23-	
38121_at	WARS	X59892	6	Pass	34.17	22.83	13	Pass	TRUE	FALSE	FALSE	16.31	2.10	trypanophyl-RNA synthetase; WARS	q31	
32877_i_at	UNK_AA3	AA324802	4	Pass	49.50	23.69	11	Pass	TRUE	FALSE	FALSE	23.64	2.09	Treacher Collins-Franceschetti syndrome 1; TCOF1	5q32-	
40596_at	TCOF1	U76366	6	Pass	22.33	4.55	12	Pass	TRUE	FALSE	FALSE	10.67	2.09	Treacher Collins-Franceschetti syndrome 1; TCOF1	q33.1	

Affy Qualifier	Affy Name	accession	sum of Present Calls	4 of 6 Present	Avg Freq RA	Sid Dev RA	sum of abs dec	7 of 13 present	Present in RA and Normal	Present in RA, Absent in Normal	Absent in RA, Present in Normal	Avg Freq RA (Normal)	Fold Change RA / Normal	Name	Chromosomes	Phosphatase
39072_at	MXII	L07648	6	Pass	28.50	13.14	13	Pass	TRUE	FALSE	FALSE	13.62	2.09	MAX-interacting protein 1; MXII	10q24-q25	
37033_s_at	GPXI	X13710	6	Pass	279.17	52.77	13	Pass	TRUE	FALSE	FALSE	133.38	2.09	glutathione peroxidase 1; GPXI	3p21.3	
32195_at	UNK_ALO	AL049450	6	Pass	14.17	5.12	13	Pass	TRUE	FALSE	FALSE	6.77	2.09	KIAA0224 gene product; KIAA0224	16	
37390_at	KIAA0224	D86977	6	Pass	13.67	2.94	13	Pass	TRUE	FALSE	FALSE	6.54	2.09	eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD); EIF3S3		
38449_at	UNK_w28	W28931	6	Pass	15.67	8.94	8	Pass	TRUE	FALSE	FALSE	7.50	2.09	ribonuclease/histogenin inhibitor RNH	11p15.5	
36187_at	RNH	X13973	6	Pass	39.50	15.10	13	Pass	TRUE	FALSE	FALSE	18.92	2.09	retention 2; RTN2		
34408_at	RTN2	AF004222	6	Pass	12.00	3.35	8	Pass	TRUE	FALSE	FALSE	5.75	2.09	sialophorm (gpL115, leukosialin, CD43); SPN	16p11.2	
36798_g_at	SPN	J04168	6	Pass	47.50	14.95	13	Pass	TRUE	FALSE	FALSE	22.77	2.09	protein phosphatase 1, regulatory (inhibitor) subunit 11; PPP1R11	6p21.3	
38412_at	PPP1R11	U53588	6	Pass	17.00	4.24	13	Pass	TRUE	FALSE	FALSE	8.15	2.08	leukocyte immunoglobulin like receptor, subfamily A (with TM domain), member 2; LILRA2	19q13.4	
34033_s_at	LILRA2	AF025531	6	Pass	33.67	18.47	13	Pass	TRUE	FALSE	FALSE	16.15	2.08	spermidine synthase; SRM	10p36-p22	
241_g_at	SRM	M64231	6	Pass	16.67	3.88	12	Pass	TRUE	FALSE	FALSE	8.00	2.08	B; SAFB	19p13	
41316_s_at	SAFB	U72355	6	Pass	20.67	5.05	13	Pass	TRUE	FALSE	FALSE	9.92	2.08	tubulin, alpha 1 (testis specific); TUBA1	2q	
36591_at	TUBA1	X06956	6	Pass	114.67	24.81	13	Pass	TRUE	FALSE	FALSE	55.08	2.08	ATP-binding cassette, sub-family F (GCN20), member 3, hypothetical protein FLJ11198; ABCF3	3q25.1-q25.2	
38830_at	ABCF3	U66685	5	Pass	9.20	3.77	7	Pass	TRUE	FALSE	FALSE	4.43	2.08	putative glioblastoma cell differentiation-related-putative glioblastoma cell differentiation-related protein; GBDRL	1	
38841_at	GBDRL	AF068195	6	Pass	9.00	4.52	12	Pass	TRUE	FALSE	FALSE	4.33	2.08	hepatitis C-associated microtubular aggregate protein (44kD); MTAP44		
37641_at	MTAP44	D28915	6	Pass	11.50	7.48	13	Pass	TRUE	FALSE	FALSE	5.54	2.08	contig. ORF: HSXO28ORF		
41838_at	UNK_X99	X99270	6	Pass	7.50	2.35	13	Pass	TRUE	FALSE	FALSE	3.62	2.07	KIAA0708 protein; KIAA0708	11q13	
41614_at	KIAA0708	AB014608	6	Pass	6.83	2.04	10	Pass	TRUE	FALSE	FALSE	3.30	2.07	multiple endocrine neoplasia 1; MEN1		
448_g_at	MEN1	U91237	6	Pass	6.83	1.83	10	Pass	TRUE	FALSE	FALSE	3.30	2.07	sortilin-related receptor, L (DLR class) A repeat-containing; SORL1	11q23.2-q24.2	
32140_at	SORL1	Y08110	6	Pass	81.00	22.91	13	Pass	TRUE	FALSE	FALSE	39.15	2.07	KIAA0323 protein; KIAA0323		
32592_at	KIAA0323	AB002321	6	Pass	17.17	4.67	13	Pass	TRUE	FALSE	FALSE	8.31	2.07	integrin, alpha X (antigen CD11C (p150), alpha polypeptide); ITGA X	16p11.2	
36709_at	ITGA X	Y00093	6	Pass	30.83	17.06	13	Pass	TRUE	FALSE	FALSE	14.92	2.07	KIAA0346 protein; KIAA0346	17p13.1	
41387_t_at	KIAA0346	AB002344	6	Pass	11.50	6.16	7	Pass	TRUE	FALSE	FALSE	5.57	2.06	thyroid hormone receptor-associated protein, 240 kDa subunit; TRAP240	17	
41625_at	TRAP240	AB011165	6	Pass	5.83	3.19	12	Pass	TRUE	FALSE	FALSE	2.83	2.06	FLN29 gene product; FLN29	12q	
35254_at	FLN29	AB007447	6	Pass	15.67	4.63	13	Pass	TRUE	FALSE	FALSE	7.62	2.06			

HuPBMC\_RA\_U95A-Kin-PhosP.xls

Atfy Qualifier	Atfy Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Sid Dev RA	sum of abs dec	Present in RA and Normal	Present in RA, Normal	Absent in RA, Normal	Fold Change RA / Normal	Name	Chromosome	Gene or Phosphate
38780_at	AKR1A1	J04794	6	Pass	28.00	8.65	13	Pass	TRUE	FALSE	13.62	aldo-keto reductase family 1, member A1 (aldehyde reductase), AKR1A1	1p33-p32	
40890_at	MTX1	U46920	6	Pass	27.83	7.55	13	Pass	TRUE	FALSE	13.54	measlin 1, MTX1	1q21	
39412_at	ZNF173	U09825	6	Pass	12.33	5.57	9	Pass	TRUE	FALSE	2.06	zinc finger protein 173; ZNF173	6p21.3	
33215_g_at	RPM312	Y11681	6	Pass	33.67	6.53	13	Pass	TRUE	FALSE	16.38	ribosomal protein, mitochondrial, S12; RPM312	19q13.1	
34310_at	APRT	Y00486	5	Pass	25.40	6.27	11	Pass	TRUE	FALSE	12.36	adenine phosphoribosyltransferase; APRT	16q24	
33409_at	FKBP2	AA158243	6	Pass	15.00	4.65	13	Pass	TRUE	FALSE	7.31	FK506-binding protein 2 (13kD); FKBP2	11q13.1-q13.3	
33748_at	KIAA0223	D86976	6	Pass	53.50	13.14	13	Pass	TRUE	FALSE	26.08	minor histocompatibility antigen HA-1; KIAA0223	19p13.3	
33323_t_at	SEF	X57348	6	Pass	11.50	4.72	13	Pass	TRUE	FALSE	5.62	stratifin; SEF	1p	
32228_at	ADT1B	AB020706	5	Pass	19.60	6.77	7	Pass	TRUE	FALSE	9.57	adaptor-related protein complex 2, alpha 2 subunit; AP2A2	11	
32236_at	UBE2G2	AF032456	6	Pass	25.17	11.18	13	Pass	TRUE	FALSE	12.31	ubiquitin-conjugating enzyme E2C 2 (homologous to yeast UBC7); UBE2G2	21q22.3	
32629_f_at	BTNSA1	U90552	6	Pass	111.33	28.98	13	Pass	TRUE	FALSE	54.46	biatrophin, subfamily 3, member A1; BTNSA1	6p22.1	
35769_at	GRP56	AJ010001	6	Pass	23.17	9.30	12	Pass	TRUE	FALSE	11.33	G protein-coupled receptor 56; GRP56	16q13	
39541_at	UNK_W52	W52003	4	Pass	12.00	4.08	8	Pass	TRUE	FALSE	5.88			
33898_at	MCRS1	AF015308	6	Pass	16.33	5.28	8	Pass	TRUE	FALSE	8.00	microspherule protein 1; MCRS1	12	
36155_at	KIAA0275	D87465	6	Pass	67.83	11.11	13	Pass	TRUE	FALSE	33.23	KIAA0275 gene product; 10		
709_at	UNK_J003	J00314	6	Pass	16.50	3.62	11	Pass	TRUE	FALSE	8.09	tubulin, beta polypeptide; TUBB	6p21.3	
37147_at	SCGF	AF020044	6	Pass	18.33	5.85	12	Pass	TRUE	FALSE	9.00	stem cell growth factor; lymphocyte secreted C-type lectin; SCGF	19q13.3	
39865_at	UNK_A18	A1890903	6	Pass	9.67	2.66	12	Pass	TRUE	FALSE	4.75			
40869_at	RBM6	AF069517	6	Pass	9.67	2.73	12	Pass	TRUE	FALSE	4.75	RNA binding motif protein 6; RBM6	3p21.3	
33282_t_at	CD81	M33680	6	Pass	77.33	22.92	13	Pass	TRUE	FALSE	38.00	CD81 antigen (target of antiproliferative antibody 1); CD81	11p15	
39141_at	ABCF1	AF027302	6	Pass	12.83	4.17	13	Pass	TRUE	FALSE	6.31	ATP-binding cassette, subfamily F (GCN20), member F; ABCF1	6p21.33	
715_s_at	GGT1	D87002	6	Pass	7.67	2.07	13	Pass	TRUE	FALSE	3.77	gamma-glutamyltransferase 1, gamma-glutamyltransferase 2; signal transducer and activator of transcription 1; STAT1	22q11.1-q11.2,22q11.23	
33338_at	STAT1	M97936	6	Pass	20.00	9.80	12	Pass	TRUE	FALSE	9.83		2q37.2	
38257_at	NDUFS8	AF038406	6	Pass	10.17	5.56	10	Pass	TRUE	FALSE	5.00	NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH-coenzyme Q reductase);	11q13	
32553_at	MAZ	M94046	6	Pass	96.33	20.40	13	Pass	TRUE	FALSE	47.38	MYC-associated zinc finger protein (purine-binding transcription	10p11.2	
1404_t_at	SCYAS	M21121	6	Pass	10.50	3.94	12	Pass	TRUE	FALSE	5.17	small inducible cytokine binding	17q11.2-q12	
37256_at	UNK_A182	A1829890	6	Pass	10.83	2.86	12	Pass	TRUE	FALSE	5.33	AS1RANTES; SCYAS	q12	

Human RA 2x or greater

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Ally Qualifier	Ally Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of 7 of 13 present	Present in RA and Normal	Present in RA, Absent in Normal	Absent in RA, Present in Normal	Avg Freq (Normal)	Fold Change RA / Normal	Name	Chromosome	Kinase or Phosphatase
40994_at	DEDD	AF043733	6	Pass	21.67	9.05	12	Pass	TRUE	FALSE	10.67	2.03	death effector domain-containing; DEDD		
38864_at	UNK_W26	W26851	6	Pass	13.00	2.00	10	Pass	TRUE	FALSE	6.40	2.03			
41267_at	KIAA1049	AB028972	6	Pass	22.33	6.95	13	Pass	TRUE	FALSE	11.00	2.03	KIAA1049 protein;	16	
32080_at	TETRA	L11669	6	Pass	42.17	12.22	13	Pass	TRUE	FALSE	20.77	2.03	tetracycline transporter-like protein; TETRA	4p16.3	
35944_at	UNK_AL0	AL031228	5	Pass	14.20	5.54	7	Pass	TRUE	FALSE	7.00	2.03	Clustered AL031228; Human DNA sequence from clone 1033B10 on chromosome 6p21.2-21.31. Contains the BING5 gene, exons 11 to 15 of the BING4 gene, the gene for GalT3 (beta3-Galactosyltransferase), the RPS18 (40S ribosomal protein S18) gene, the SACM2L (suppressor of actin mutation 2, yeast, homolog) gene, a pseudogene similar to TAT-SF1, a Pseudogene similar to zinc finger genes, the RING1 gene, the gene for HKE6 (RING2), the gene for HKE4 (RING5), the RXRB (Retinoid X receptor beta) gene, the COL1A2 (collagen, type XI, alpha 2) gene, the HLA-DPB2 pseudogene and part of the HLA-DPA3 pseudogene. Contains predicted CpG	6p21.3	
33388_at	UNK_AL0	AL080223	6	Pass	22.00	5.40	13	Pass	TRUE	FALSE	10.85	2.03			
40787_at	UNK_U90	U90911	6	Pass	12.17	3.66	13	Pass	TRUE	FALSE	6.00	2.03			
35911_at	MMP1	AL003147	6	Pass	24.50	8.14	12	Pass	TRUE	FALSE	12.08	2.03	matrix metalloproteinase-like 1; MMP1	16p13.3	
37003_at	CD63	X62654	6	Pass	29.00	14.71	13	Pass	TRUE	FALSE	14.31	2.03	CD63 antigen (melanoma antigen); CD63	12q12-q13	
38475_at	DCTN-50	U50733	6	Pass	14.50	5.54	13	Pass	TRUE	FALSE	7.15	2.03	dynamitin (dynactin complex, 50 kD subunit); DCTN-50	12	
870_f_at	MT3	M03311	6	Pass	31.50	13.44	11	Pass	TRUE	FALSE	15.55	2.03	metallothionein 3 (growth inhibitory factor (neurotrophic)); MT3	16q13	
34178_at	UNK_A188	A1884738	6	Pass	7.17	1.60	13	Pass	TRUE	FALSE	3.54	2.03	zinc finger protein 297; ZNF297	6p21.3	
36167_at	ATP6F	D89052	6	Pass	64.50	29.51	13	Pass	TRUE	FALSE	31.85	2.03	ATPase, H+ transporting; lysosomal (vacuolar proton pump) 21kD; syntaxin 4A (placental); STX4A	1p32.3	
37911_at	STX4A	U07158	6	Pass	13.33	3.88	12	Pass	TRUE	FALSE	6.58	2.03			
38523_c_at	U2AFIR3	D49677	6	Pass	13.67	2.58	12	Pass	TRUE	FALSE	6.75	2.02	U2 small nuclear ribonucleoprotein auxiliary factor, small subunit 2; U2AFIR3	Xp22.1	
37931_at	CENPB	X05299	6	Pass	10.67	2.42	11	Pass	TRUE	FALSE	5.27	2.02	centromere protein B (80kD); CENPB	20p13	
35124_at	ALOX12	M62982	6	Pass	14.00	4.69	13	Pass	TRUE	FALSE	6.92	2.02	arachidonate 12-lipoxygenase; ALOX12	17p13.1	

Affy Qualifier	Affy Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of 7 of 13 abs dec	Present in RA and Normal	Present in RA, Absent in Normal	Avg Freq (Normal)	Fold Change RA / Normal	Name	Chromosome	Kinase or Phosphatase	
32523_at	CLTB	M20470	6	Pass	5.17	1.83	9	Pass	TRUE	FALSE	2.56	2.02	elastin, light polypeptide (LzB); CLTB	4q2-q3	
37442_at	UNK_AL0	AL050378	6	Pass	18.00	6.32	13	Pass	TRUE	FALSE	8.92	2.02	oxoglutarate dehydrogenase	7p14-p13	
40470_at	OGDH	D10523	5	Pass	14.40	3.85	7	Pass	TRUE	FALSE	7.14	2.02	lysosomal-associated multispanning membrane protein-5; LAPTM5	1p34	
37759_at	LAPTM5	U51240	6	Pass	229.50	56.06	13	Pass	TRUE	FALSE	113.85	2.02	SSAL		
37126_at	SSA1	M62800	5	Pass	15.00	5.83	9	Pass	TRUE	FALSE	7.44	2.01	Sjogren syndrome antigen A1 (SjA), ribonucleoprotein autoantigen SS-A/Ro);	11p15.5	
34260_at	KIAA0683	AB014583	5	Pass	6.80	2.49	8	Pass	TRUE	FALSE	3.38	2.01	KIAA0683 gene product;	16	
1468_at	TRAP1	U12595	6	Pass	11.00	2.10	13	Pass	TRUE	FALSE	5.46	2.01	heat shock protein 75; TRAP1	16	
37272_at	ITPKB	X57206	6	Pass	28.50	6.38	13	Pass	TRUE	FALSE	14.15	2.01	inositol 1,4,5-bisphosphate 3-kinase B; transforming growth factor, beta 1; TGFBI	1q41-q43	kinase
1830_s_at	TGFBI	M38449	6	Pass	30.67	6.80	13	Pass	TRUE	FALSE	15.23	2.01	ring finger protein 1; RING1	19q13.1	
35685_at	RING1	Z14000	6	Pass	15.33	3.93	13	Pass	TRUE	FALSE	7.62	2.01	v-red avian reticulendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3)	6p21.3	
1295_at	RELA	L19067	6	Pass	39.17	15.38	13	Pass	TRUE	FALSE	19.46	2.01	FOS-like antigen-1; FOSL1	11q13	
32271_at	FOSL1	X16707	4	Pass	9.25	2.75	10	Pass	TRUE	FALSE	4.60	2.01	acycloxycyl hydrolase (neutrophil); AOAH	11q13	
34435_at	AQP9	AB008775	6	Pass	7.83	5.19	10	Pass	TRUE	FALSE	3.90	2.01	prostatic binding protein; PRBP	7p14-p12	
37647_at	AOAH	M62840	6	Pass	25.00	14.34	13	Pass	TRUE	FALSE	12.46	2.01	MYC promoter-binding protein 1, enolase 1, (alpha); ENO1, MPB1	1p36.1	
32611_at	PBP	X75232	6	Pass	14.50	5.09	13	Pass	TRUE	FALSE	7.23	2.01	capping protein (actin filament) muscle Z-line, beta; CAPZB	1p36.1	
2035_s_at	MPB1	M55914	6	Pass	125.67	55.44	13	Pass	TRUE	FALSE	62.69	2.00	MAP-kinase activating death domain; MADD	1p36.3-p36.2,1p36.1	
37012_at	CAPZB	U03271	6	Pass	65.83	19.11	13	Pass	TRUE	FALSE	32.85	2.00	KIAA0140 gene product; KIAA0140	1p36.3	
34830_at	UNK_W25	W25986	6	Pass	36.83	7.31	13	Pass	TRUE	FALSE	18.38	2.00	Src-like adapter, SLA	1p35	
38398_at	MADD	AB002356	6	Pass	16.33	6.09	13	Pass	TRUE	FALSE	8.15	2.00	tetratricopeptide repeat domain 2, TTC2	1p36.1	
40143_at	KIAA0140	D50930	6	Pass	18.33	7.23	13	Pass	TRUE	FALSE	9.15	2.00	capillary renal cell carcinoma (translocation-associated); PRCC	11p11.2	
35205_at	DRKZF586	AL050280	6	Pass	32.50	9.40	13	Pass	TRUE	FALSE	16.23	2.00	Solute carrier family 19 protein; DKFZF5860519 protein; DKFZF5860519		
1427_g_at	SLA	D89077	6	Pass	22.33	10.86	13	Pass	TRUE	FALSE	11.15	2.00	Src-like adapter, SLA	8q24	
41800_s_at	TTC2	U46571	6	Pass	22.33	5.65	13	Pass	TRUE	FALSE	11.15	2.00	tetratricopeptide repeat domain 2, TTC2	17q11.2	
39149_at	PRCC	X99720	6	Pass	10.00	2.00	7	Pass	TRUE	FALSE	5.00	2.00	papillary renal cell carcinoma (translocation-associated); PRCC	1q21.1	
41778_at	SLC1A5	U53347	5	Pass	8.00	3.61	8	Pass	TRUE	FALSE	4.00	2.00	solute carrier family 1 (neutral amino acid transporter), member 5; SLC1A5	19q13.3	
40149_at	DRKZF547	AL049924	6	Pass	7.00	0.63	8	Pass	TRUE	FALSE	3.50	2.00	SH2-B homolog; SH2B		

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Atty Qualifier	Atty Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of abs present dec	Present in RA and Normal	Present in RA, Absent in Normal	Absent in RA, Present in Normal	Avg Freq (normal) RA / Normal	Fold Change RA / Normal	Name	Cytosolic or Phosphatase
453_at	SMARCC2	U66616	6	Pass	5.00	2.00	8	Pass	TRUE	FALSE	2.50	2.00	SWI/SNF related, matrix associated, actin dependent (SMARCC2)	12q13-q14
40840_at	PPIF	M80254	6	Pass	8.67	2.66	9	Pass	TRUE	FALSE	4.33	2.00	peptidylprolyl isomerase F subfamily c, member 2; PPIF	10q22-q23
1014_at	POLG	U60325	6	Pass	10.00	3.41	12	Pass	TRUE	FALSE	5.00	2.00	polynucleotide phosphorylase (DNA directed), gamma; POLG	15q25
1243_at	DDX2	U18300	6	Pass	11.00	1.79	12	Pass	TRUE	FALSE	5.50	2.00	damage-specific DNA binding protein 2 (48KD); DDX2	11p12-p11
1487_at	ESRRA	L38487	6	Pass	12.00	5.18	12	Pass	TRUE	FALSE	6.00	2.00	estrogen-related receptor alpha; ESRRA	11q12
197_at	NME3	U29656	6	Pass	10.50	2.88	12	Pass	TRUE	FALSE	5.25	2.00	non-metastatic cells 3; protein expressed in; NME3	16q13
32533_s_at	VAMP5	AF054825	6	Pass	9.50	4.23	12	Pass	TRUE	FALSE	4.75	2.00	vesicle-associated membrane protein 5 (synovial); VAMP5	
34871_at	UNK_W3C	W30677	6	Pass	18.67	6.83	12	Pass	TRUE	FALSE	9.33	2.00		
36815_at	UNK_AFO	AF038185	6	Pass	16.00	3.41	12	Pass	TRUE	FALSE	8.00	2.00		
40282_s_at	DF	M84526	6	Pass	38.00	25.78	13	Pass	TRUE	FALSE	19.00	2.00	D component of complement (adipsin); DF	19
36645_at	RELA	L19067	6	Pass	33.67	12.82	13	Pass	TRUE	FALSE	16.85	2.00	v-rel avian reiculoendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (ngf3)); RELA	11q13
41471_at	S100A9	W72424	6	Pass	313.50	166.70	13	Pass	TRUE	FALSE	157.00	2.00	S100 calcium-binding protein A9 (calgranulin B); S100A9	1q21
33227_at	IL10RB	A1984234	6	Pass	15.33	6.22	13	Pass	TRUE	FALSE	7.69	1.99	interleukin 10 receptor, beta; IL10RB	21q22.11
38308_s_at	KIAA0607	AB011179	6	Pass	30.50	9.31	13	Pass	TRUE	FALSE	15.31	1.99	neurochondrin; KIAA0607	1
36145_at	SLAHBP1	U51586	6	Pass	22.50	6.77	13	Pass	TRUE	FALSE	11.31	1.99	siah binding protein 1; siah binding protein 1; FBP interacting repressor; pyrimidine tract binding splicing factor; Ro ribonucleoprotein-binding protein 1; SLAHBP1	8q24.2-qel
40469_at	MCM3AP	AB011144	6	Pass	22.50	6.66	13	Pass	TRUE	FALSE	11.31	1.99	minichromosome maintenance deficient (S. cerevisiae) 3-associated protein; MCM3AP	21q22.3
1506_at	IL2RG	D11086	6	Pass	26.33	8.02	12	Pass	TRUE	FALSE	13.25	1.99	interleukin 2 receptor, gamma (severe combined immunodeficiency); IL2RG	Xq13.1
33781_s_at	UBE2M	AF075599	6	Pass	6.50	2.43	11	Pass	TRUE	FALSE	3.27	1.99	ubiquitin-conjugating enzyme E2M (homologous to yeast UBC12); UBE2M	
40501_s_at	MYBPC1	X73114	5	Pass	14.20	4.44	13	Pass	TRUE	FALSE	7.15	1.98	myosin-binding protein C; 12 slow-type MYBPC1	12
35267_s_at	BC10	AL049288	6	Pass	14.33	4.93	13	Pass	TRUE	FALSE	7.23	1.98	bladder cancer associated protein; BLCAP	20
36959_at	UBE2V1	U49278	6	Pass	25.00	9.98	13	Pass	TRUE	FALSE	12.62	1.98	hypothetical protein DKFZp547H084.ubiquitin-conjugating enzyme E2 variant 1; UBE2V1	20q13.2
32967_at	TOSO	AF057557	6	Pass	23.00	7.46	13	Pass	TRUE	FALSE	11.62	1.98	regulator of Fas-induced apoptosis; TOSO	

Atty Qualifier	Atty Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of abs dec	Present in RA and Normal	Present in RA, Absent in Normal	Absent in RA, Present in Normal	Avg Freq (Normal)	Ratio Change RA / Normal	Name	Chromosome	Kinase or Phosphatase
38138_at	RRAS	AI201108	6	Pass	15.83	5.53	12	Pass	TRUE	FALSE	8.00	1.98	related RAS viral (r-ras) oncogene homolog; RRAS	19q13.1	
34892_at	TNFRSF10	AF016266	6	Pass	15.83	5.49	13	Pass	TRUE	FALSE	8.00	1.98	tumor necrosis factor receptor superfamily member 10b; TNFRSF10B	8p22-p21	
38181_at	MAP11	X37766	6	Pass	11.33	4.41	11	Pass	TRUE	FALSE	5.73	1.98	matrix metalloproteinase 11 (stromelysin 3); KIAA0674	22q11.23	
31826_at	KIAA0674	AB014574	6	Pass	28.00	9.40	13	Pass	TRUE	FALSE	14.15	1.98	KIAA0674 protein; KIAA0674	9	
34347_at	DKFZP564I04955		6	Pass	22.67	5.24	13	Pass	TRUE	FALSE	11.46	1.98	DKFZP564I0123 protein; DKFZP564I0123	3p21.2-24.2	
40076_at	TPD52L2	AF004430	6	Pass	22.67	11.27	13	Pass	TRUE	FALSE	11.46	1.98	tumor protein D52-like 2; TPD52L2	20q13.2-q13.3	
37967_at	D6S49E	AF000424	6	Pass	100.17	51.60	13	Pass	TRUE	FALSE	50.69	1.98	DNA segment on chromosome 6 (unique) 49 expressed sequence; D6S49E Homo sapiens LST1 mRNA	6p21.3	
37487_at	KIAA1093	AB029016	6	Pass	10.33	3.88	13	Pass	TRUE	FALSE	5.23	1.98	KIAA1093 protein; KIAA1093	22	
41522_at	MFNG	Z93096	6	Pass	10.33	3.72	13	Pass	TRUE	FALSE	5.23	1.98	manic fringe (Drosophila) homolog; MFNG	22q12	
36637_at	ANXA11	L19605	6	Pass	25.83	7.41	13	Pass	TRUE	FALSE	13.08	1.98	annexin A11; ANXA11	10q22-q23	
553_g_at	ARHGAP1	U02570	6	Pass	43.00	15.65	13	Pass	TRUE	FALSE	21.77	1.98	Rho GTPase activating protein 1; ARHGAP1		
33201_at	SSNA1	Z96932	4	Pass	19.50	7.19	8	Pass	TRUE	FALSE	9.88	1.97	Syngren's syndrome nuclear autoantigen 1; fusion, derived from t(12;16) malignant liposarcoma; FUS	16p11.2	
39180_at	FUS	S62140	6	Pass	47.83	13.29	13	Pass	TRUE	FALSE	24.23	1.97	inertidekin 10 receptor, alpha; IL10RA	11q23	
1062_g_at	IL10RA	U00672	6	Pass	47.67	15.71	13	Pass	TRUE	FALSE	24.15	1.97	Homo sapiens LST1 mRNA		
41375_at	UNK_AJ24	AJ245416	6	Pass	15.17	5.88	13	Pass	TRUE	FALSE	7.69	1.97	death-associated protein; DAP	5p15.2	
36199_at	DAP	X76105	6	Pass	21.67	3.88	12	Pass	TRUE	FALSE	11.00	1.97	calumenin; CALU	7q32	
37345_at	CALU	AF013759	5	Pass	6.40	1.14	12	Pass	TRUE	FALSE	3.25	1.97	clathrin, light polypeptide (Lca); CLTA	12q23-q24	
38657_s_at	CLTA	M20471	6	Pass	43.17	19.93	13	Pass	TRUE	FALSE	21.92	1.97	carcinoembryonic antigen-related cell adhesion molecule 4; CEACAM4	19q13.2	
32490_at	CEACAM4	AC005955	5	Pass	9.00	2.92	7	Pass	TRUE	FALSE	4.57	1.97	structure specific recognition protein 1; SSRP1	11q12	
37739_at	SSRP1	M86737	6	Pass	16.50	4.55	13	Pass	TRUE	FALSE	8.38	1.97	benzodiazepine receptor (peripherally); BZRP	22q13.31	
32806_at	BZRP	M36035	6	Pass	248.17	116.68	13	Pass	TRUE	FALSE	126.15	1.97	chitinase 3-like 2; CHI3L2	1p13.3	
31891_at	CHI3L2	U58515	6	Pass	6.33	1.51	9	Pass	TRUE	FALSE	3.22	1.97	nardilysin (N-arginine dihydrolase); NRD1	1p32.2-p32.3	
31801_at	UNK_A180	A1808712	6	Pass	13.00	6.26	13	Pass	TRUE	FALSE	6.62	1.96	procollagen-proline, 2-oxoglutarate 4-hydroxylase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase); thymoid hormone binding		
34787_at	NRD1	X93209	6	Pass	32.17	9.64	13	Pass	TRUE	FALSE	16.38	1.96	small nuclear ribonucleoprotein A1; SNRPA	19q13.1	
36666_at	P4HB	M22806	6	Pass	77.17	21.94	13	Pass	TRUE	FALSE	39.31	1.96			
39738_at	APOL	Z82215	6	Pass	152.17	26.57	13	Pass	TRUE	FALSE	77.62	1.96			
40842_at	SNRPA	M60784	6	Pass	36.17	8.80	13	Pass	TRUE	FALSE	18.46	1.96			

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39551_at	UNK_N98	N98667	6	Pass	25.00	9.57	13	TRUE	FALSE	FALSE	12.77	1.96	hypothetical protein: LOC51317		
35017_t_at	UNK_M80	M80469	6	Pass	129.67	39.72	13	TRUE	FALSE	FALSE	66.23	1.96	Cluster Incl M80469: Human MHC class I (HLA-J gene, exons 1-8 and complete cds.		
894_g_at	E2-EPF	M91670	6	Pass	13.50	4.85	10	TRUE	FALSE	FALSE	6.90	1.96	ubiquitin carrier protein: E2-EPF	17	
590_at	ICAM2	M32334	6	Pass	26.33	4.72	13	TRUE	FALSE	FALSE	13.46	1.96	intercellular adhesion molecule 2; ICAM2	17q23-q25	
34346_at	PRKAG1	U24212	6	Pass	16.83	6.01	13	TRUE	FALSE	FALSE	8.62	1.95	protein kinase, AMP-activated, gamma 1 non-catalytic subunit;	12q12-q14	
39500_s_at	UNK_AL0	AL049299	5	Pass	8.40	2.70	10	TRUE	FALSE	FALSE	4.30	1.95	NADH dehydrogenase (ubiquinone) Fe-S protein		
34865_at	NDUFS6	AI360249	5	Pass	9.60	4.34	12	TRUE	FALSE	FALSE	4.92	1.95	6 (13kD) (NADH-coenzyme Q reductase)		
37344_at	HLA-DMA	X62744	6	Pass	51.50	18.12	13	TRUE	FALSE	FALSE	26.38	1.95	major histocompatibility complex, class II, DM alpha; HLA-DMA	6p21.3	
34692_t_at	ARPC4	AF006087	6	Pass	22.67	7.84	13	TRUE	FALSE	FALSE	11.62	1.95	actin related protein 2/3 complex, subunit 4 (20 kD); ARPC4		
41776_at	ATOX1	U70660	6	Pass	13.33	4.50	12	TRUE	FALSE	FALSE	6.83	1.95	ATX1 (antioxidant protein 1; yeast) homolog 1; ATOX1	5q32	
34885_at	SYNGR2	AJ002108	6	Pass	75.17	17.66	13	TRUE	FALSE	FALSE	38.54	1.95	synaptogyrin 2; SYNGR2	17qter	
893_at	E2-EPF	M91670	5	Pass	7.80	1.79	9	TRUE	FALSE	FALSE	4.00	1.95	ubiquitin carrier protein: E2-EPF	17	
33956_at	MD-2	AB018549	6	Pass	13.50	2.89	13	TRUE	FALSE	FALSE	6.92	1.95	MD-2 protein; MD-2	8	
38725_s_at	DPN2	N36295	6	Pass	10.50	3.56	13	TRUE	FALSE	FALSE	5.38	1.95	dolichyl-phosphate mannosyltransferase polypeptide 2, regulatory subunit; DPN2		
40938_at	DKFZP564	W26496	6	Pass	10.50	8.41	13	TRUE	FALSE	FALSE	5.38	1.95	DKFZP564A122 protein; DKFZP564A122		
39811_at	UNK_AA4	AA402538	6	Pass	26.83	8.45	13	TRUE	FALSE	FALSE	13.77	1.95	small inducible cytokine A3 (homologous to mouse Mip-1b); SCYA3	17q11-q21	
36103_at	SCYA3	D90144	6	Pass	6.33	2.80	12	TRUE	FALSE	FALSE	3.25	1.95	poly(pyrrolidine) tract binding protein (heterogeneous nuclear ribonucleoprotein U); PTB	14q21-q24.1	
40593_at	PTB	X66975	6	Pass	64.00	23.03	13	TRUE	FALSE	FALSE	32.85	1.95	poly(pyrrolidine) tract binding protein (heterogeneous nuclear ribonucleoprotein U); PTB	14q21-q24.1	
1532_g_at	UNK_U50	U50535	6	Pass	16.33	3.44	13	TRUE	FALSE	FALSE	8.38	1.95	human BRCA2 region; mRNA sequence CC006		
32264_at	UNK_L23	L23134	5	Pass	29.60	14.67	10	TRUE	FALSE	FALSE	15.20	1.95	granzyme M (lymphocyte met-enkephalin); GZMM	19p13.3	
1097_a_at	CCR7	L31584	6	Pass	44.33	27.45	13	TRUE	FALSE	FALSE	22.77	1.95	chemokine (C-C motif) receptor 7; CCR7	17q12-q21.2	
33753_at	PRP8	AB007510	6	Pass	56.00	9.06	13	TRUE	FALSE	FALSE	28.77	1.95	U5 snRNP-specific protein (220 kD), ortholog of S. cerevisiae Prp8; PRP8	17p13.3	
36129_at	UNK_AB0	AB007857	6	Pass	25.00	4.69	13	TRUE	FALSE	FALSE	12.85	1.95	KIAA0397 gene product; KIAA0397		
33367_s_at	LOC51582	D88674	6	Pass	4.33	2.34	10	TRUE	FALSE	FALSE	8.50	-1.96	antizyme inhibitor; protease, serine; 15; LOC51582; PRSS15	19p13.2,8	
AFFX-M27831	26SRNAS	M27830	6	Pass	9.17	6.01	13	TRUE	FALSE	FALSE	18.46	-2.01	#N/A	#N/A	



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34642_at	YWHAZ	U28964	6	Pass	15.17	10.83	13	Pass	TRUE	FALSE	30.62	-2.02	lysine 3-monooxygenase/tyrosine 3-monooxygenase activation protein, zeta polypeptide; YWHAZ	2p25.2-p25.1	

qualifier	name	sum of abs dec	4 of 6 present	Avg Freq Std Dev RA	sum of 7 of 13 abs present and dec	Present in RA and Normal	Present in RA, Absent in Normal	Avg Freq (Normal )	Fold Change RA/Normal	Name	Chromos- ome
1642_at	MTA1	U35113	4	Pass	4.75 1.26	0 Fail	FALSE	TRUE	#DIV/0!	metastasis associated 1; MTA1	
37963_at	AKSA	X52151	4	Pass	3.50 1.73	0 Fail	FALSE	TRUE	#DIV/0!	arabidopsis A; AKSA	22q13.33
38350_f_at	TUBA2	AF003392	4	Pass	10.25 1.26	0 Fail	FALSE	TRUE	#DIV/0!	tubulin, alpha 2; TUBA2	13q11
40800_at	UNK_A159	A1590869	4	Pass	6.75 1.71	0 Fail	FALSE	TRUE	#DIV/0!	hypothetical protein similar to mouse Hn1 (Hematological and Neurological expressed sequence 1); HN1L	16
38021_at	PLEC1	U53204	6	Pass	22.17 10.91	0 Fail	FALSE	TRUE	#DIV/0!	plectin 1, intermediate filament binding protein, 50KDa; PLEC1	8q24
1257_s_at	QSCN6	L42379	4	Pass	19.00 18.57	1 Fail	FALSE	TRUE	6.33	quiescin Q6; QSCN6	1q24
39128_f_at	PPP2R4	X73478	4	Pass	7.25 5.68	2 Fail	FALSE	TRUE	1.50 4.83	protein phosphatase 2A, regulatory subunit B' (PR 53); PPP2R4	9q34
545_g_at	NFKB2	S76638	4	Pass	4.50 1.29	1 Fail	FALSE	TRUE	1.00 4.50	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100); NFKB2	11q24
37769_at	EDG4	AF011466	6	Pass	20.50 4.32	1 Fail	FALSE	TRUE	5.00 4.10	endothelial differentiation, lysophosphatidic acid G- protein-coupled receptor, 4; EDG4	19p12
2049_s_at	JUNB	M29039	5	Pass	10.80 7.19	6 Fail	FALSE	TRUE	2.67 4.05	jun B proto-oncogene; JUNB	19p13.2
39145_at	MYRL2	J02854	6	Pass	19.33 9.24	1 Fail	FALSE	TRUE	5.00 3.87	myosin regulatory light chain 2, smooth muscle isoform; MYRL2	
32151_at	RANGAP1	X82260	4	Pass	12.25 2.63	2 Fail	FALSE	TRUE	3.50 3.50	Ran GTPase activating protein 1; RANGAP1	22q13.2- q13.31
34367_at	PHGDH	AF006043	6	Pass	5.83 3.43	3 Fail	FALSE	TRUE	1.67 3.50	3-phosphoglycerate dehydrogenase; PHGDH	1p11.1- 13.1
31596_f_at	UNK_L023	L02326	6	Pass	46.50 17.20	4 Fail	FALSE	TRUE	13.50 3.44	immunoglobulin lambda- like polypeptide 2; IGL2	22q11.23
34105_f_at	UNK_A114	A1147237	4	Pass	53.75 31.42	6 Fail	FALSE	TRUE	15.67 3.43	endothelial cell growth factor 1 (platelet-derived); ECGF1	22q13.33
1665_s_at	ECGF1	M63193	4	Pass	77.75 68.10	3 Fail	FALSE	TRUE	23.33 3.33	endothelial cell growth factor 1 (platelet-derived); ECGF1	
1855_at	FGF3	X14445	4	Pass	6.50 2.65	3 Fail	FALSE	TRUE	2.00 3.25	fibroblast growth factor 3 (murine mammary tumor virus integration site (v-int 2) oncogene homolog); FGF3	11q13
36151_at	HU-K4	U60644	5	Pass	13.00 4.47	5 Fail	FALSE	TRUE	4.00 3.25	similar to vaccinia Hijrid III K4; ORF; HU-K4	
32133_at	PIP5K1C	AB011161	6	Pass	14.67 5.99	5 Fail	FALSE	TRUE	4.60 3.19	phosphatidylinositol-4- phosphate 5-kinase, type I, gamma; PIP5K1C	19

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41659_at	SUPT6H	U46691	4	Pass	4.50	2.38	2 Fail	FALSE	TRUE	FALSE	1.50	3.00	suppressor of Ty (S.cerevisiae) 6 homolog; SUPT6H	17q11.2	
36158_at	DCTN1	AF086947	5	Pass	7.80	1.92	5 Fail	FALSE	TRUE	FALSE	2.60	3.00	dynactin 1 (p150, Glued (Drosophila) homolog); DCTN1	2p13	
35916_g_at	CPT1B	Y08683	5	Pass	8.00	2.35	4 Fail	FALSE	TRUE	FALSE	2.75	2.91	carnitine palmitoyltransferase 1, muscle; CPT1B	22q13.33	
41458_at	KIAA0467	AB007936	4	Pass	14.50	5.20	1 Fail	FALSE	TRUE	FALSE	5.00	2.90	KIAA0467 protein; KIAA0467	1	
33719_at	UNK_AFO	AF010242	4	Pass	8.50	1.73	2 Fail	FALSE	TRUE	FALSE	3.00	2.83	protease, serine, 16 (thymus); PRSS16	6p21	
39106_at	PRSS16	AF052514	4	Pass	8.50	3.51	2 Fail	FALSE	TRUE	FALSE	3.00	2.83	protease, serine, 16 (thymus); PRSS16	6p21	
37365_at	HSJ1	X63368	4	Pass	7.75	2.22	4 Fail	FALSE	TRUE	FALSE	2.75	2.82	heat shock protein, neuronal DNAJ-like 1; HSJ1	2q32-q34	
40951_at	UNK_ALO	AL049250	5	Pass	6.40	5.50	3 Fail	FALSE	TRUE	FALSE	2.33	2.74			
41351_at	UNK_AAS	AA885106	4	Pass	26.25	7.85	6 Fail	FALSE	TRUE	FALSE	9.83	2.67			
35228_at	CPT1B	Y08682	5	Pass	9.60	2.88	5 Fail	FALSE	TRUE	FALSE	3.60	2.67	carnitine palmitoyltransferase 1, muscle; CPT1B	22q13.33	
40165_at	UNK_ABO	AB015345	6	Pass	5.33	1.63	5 Fail	FALSE	TRUE	FALSE	2.00	2.67			
40159_f_at	NCF1	M55067	6	Pass	70.83	52.24	5 Fail	FALSE	TRUE	FALSE	26.80	2.64	neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1); NCF1	7q11.23	
39837_s_at	UNK_ACO	AC004877	4	Pass	14.50	8.74	4 Fail	FALSE	TRUE	FALSE	5.50	2.64			
33374_at	C2	L09708	4	Pass	5.25	0.96	1 Fail	FALSE	TRUE	FALSE	2.00	2.63	complement component 2; C2	6p21.3	
2009_at	PTK2B	U33284	4	Pass	5.25	1.50	2 Fail	FALSE	TRUE	FALSE	2.00	2.63	protein tyrosine kinase 2 beta; PTK2B	8p21.1	Kinase
41083_at	UNK_ACO	AC006276	4	Pass	5.25	1.71	3 Fail	FALSE	TRUE	FALSE	2.00	2.63			
37636_at	SCAP	D83782	5	Pass	11.00	3.94	4 Fail	FALSE	TRUE	FALSE	4.25	2.59	SREBP CLEAVAGE-ACTIVATING PROTEIN; SCAP	3	
100_g_at	RABGGT7	Y08200	5	Pass	9.40	4.16	3 Fail	FALSE	TRUE	FALSE	3.67	2.56	Rab geranylgeranyltransferase, alpha subunit; RABGGT7	14q11.2	
41648_at	CRAT	X78706	4	Pass	20.50	3.11	4 Fail	FALSE	TRUE	FALSE	8.00	2.56	carnitine acetyltransferase; CRAT	9q34.1	
37977_at	PMS2L11	A1138834	4	Pass	7.25	3.30	6 Fail	FALSE	TRUE	FALSE	2.83	2.56	posmeiotic segregation increased 2-like 11; PMS2L11	7q	
37491_at	TAF2A	D90359	4	Pass	15.75	6.99	6 Fail	FALSE	TRUE	FALSE	6.17	2.55	TATA box binding protein (TBP)-associated factor, RNA polymerase II, A, 250kD; TAF2A	Xq13.1	
31410_at	TAC1	AF023614	4	Pass	7.00	4.08	4 Fail	FALSE	TRUE	FALSE	2.75	2.55	transcription activator and CAML interactor; TAC1		
37360_at	LY6E	U66711	5	Pass	50.80	41.61	2 Fail	FALSE	TRUE	FALSE	20.00	2.54	lymphocyte antigen 6 complex, locus E; LY6E	8q24.3	
35434_at	MEF2D	L16794	6	Pass	6.33	1.75	6 Fail	FALSE	TRUE	FALSE	2.50	2.53	MADS box transcription enhancer factor 2, polypeptide D (myocyte enhancer factor 2D); MEF2D	1q12-q23	
38971_f_at	NAF1	AJ011896	4	Pass	53.50	25.51	5 Fail	FALSE	TRUE	FALSE	21.20	2.52	Net-associated factor 1; NAF1	5q32-q33.1	
36958_at	ZFX	X95735	6	Pass	42.83	22.68	4 Fail	FALSE	TRUE	FALSE	17.00	2.52	ZFX; ZFX	7q32	
34432_at	SH2D2A	AF051325	5	Pass	4.60	3.71	6 Fail	FALSE	TRUE	FALSE	1.83	2.51	SH2 domain protein 2A; SH2D2A	1q21	

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35194_at	GPX2	X53463	4	Pass	5.00	1.63	1 Fail	FALSE	TRUE	2.00	2.50	glutathione peroxidase 2 (cytosolic); GPX2	14q24.1	
38276_at	NFKBIE	U91616	4	Pass	5.00	0.82	1 Fail	FALSE	TRUE	2.00	2.50	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon		
40191_s_at	UNK_A176	A1761647	5	Pass	5.00	2.00	1 Fail	FALSE	TRUE	2.00	2.50	KIAA0582 protein; 2	2	
35079_at	NR3	AB003592	4	Pass	5.00	0.82	4 Fail	FALSE	TRUE	2.00	2.50	contactin 6; CNTN6	3p26-p25	
36598_s_at	INPPL1	L36818	6	Pass	9.17	4.07	6 Fail	FALSE	TRUE	3.67	2.50	inositol polyphosphate phosphatase-like 1; INPPL1	11q23	Phosphatase
35601_at	UNK_L006	L00022	6	Pass	16.83	9.47	6 Fail	FALSE	TRUE	6.83	2.46			
37719_at	MLF2	AF070539	4	Pass	11.00	3.56	2 Fail	FALSE	TRUE	4.50	2.44	myeloid leukemia factor 2; MLF2	12p13	
38464_at	GCS1	X87337	5	Pass	12.20	3.42	4 Fail	FALSE	TRUE	5.00	2.44	glucosylase 1; GCS1	2p13-p12	
40639_at	SCO2	AL021683	4	Pass	14.50	10.63	1 Fail	FALSE	TRUE	6.00	2.42	SCO (cytochrome oxidase deficient, yeast) homolog 2; SCO2	22q13.33	
41273_at	UNK_AL0	AL040940	4	Pass	6.25	0.50	5 Fail	FALSE	TRUE	2.60	2.40			
35961_at	UNK_AL0	AL040930	5	Pass	4.80	1.10	4 Fail	FALSE	TRUE	2.00	2.40			
38721_at	HBP1	W72733	6	Pass	8.50	1.22	5 Fail	FALSE	TRUE	3.60	2.36	HMG-box containing protein 1; HBP1	7q31.1	
519_g_at	NR1H2	U07132	6	Pass	25.17	7.57	3 Fail	FALSE	TRUE	10.67	2.36	nuclear receptor subfamily 1, group H, member 2; NR1H2	19q13.3-19q13.3	
41127_at	SLC1A4	L14595	5	Pass	6.20	2.28	6 Fail	FALSE	TRUE	2.67	2.33	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4; SLC1A4	2p15-p13	
38340_at	KIAA0655	AB014555	4	Pass	12.75	3.20	6 Fail	FALSE	TRUE	5.50	2.32	homingin interacting protein-1-related; KIAA0655	12q24	
32177_s_at	GAPL	AC004084	4	Pass	9.25	2.22	2 Fail	FALSE	TRUE	4.00	2.31	GTPase activating protein; GAPL	7q22-q31.1	
736_f_at	POM121L	D87002	4	Pass	10.00	2.58	3 Fail	FALSE	TRUE	4.33	2.31			
1550_at	MAAT1	U19796	4	Pass	8.00	2.45	2 Fail	FALSE	TRUE	3.50	2.29	melanoma-associated antigen recognised by T lymphocytes; MAAT1		
37945_at	HBACH	U91316	4	Pass	6.25	1.71	4 Fail	FALSE	TRUE	2.75	2.27	cytosolic acyl coenzyme A thioester hydrolase; HBACH	1p36.31-p36.11	
31822_at	CUTL1	L12579	5	Pass	9.40	3.29	6 Fail	FALSE	TRUE	4.17	2.26	cut (Drosophila)-like 1 (CCAAT displacement protein); CUTL1	7q22	
33105_at	UNK_W28	W28790	4	Pass	5.25	2.63	3 Fail	FALSE	TRUE	2.33	2.25			
33149_at	TNFRSF5	A1865431	4	Pass	6.75	3.59	6 Fail	FALSE	TRUE	3.00	2.25	tumor necrosis factor receptor superfamily, member 5; TNFRSF5	20q12-q13.2	
40619_at	E2-EPF	M91670	4	Pass	8.50	1.00	6 Fail	FALSE	TRUE	3.83	2.22	ubiquitin carrier protein; E2-EPF	17	
570_at	RELB	M83221	6	Pass	8.00	3.35	6 Fail	FALSE	TRUE	3.67	2.18	v-rel avian recombination-activating protein; oncogene homolog B (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3); RELB		
1007_s_at	DDR1	U48705	4	Pass	6.00	3.37	4 Fail	FALSE	TRUE	2.75	2.18	discoidin domain receptor family, member 1; DDR1	6p21.3	Kinase
36856_at	UNK_W28	W28743	5	Pass	13.80	6.72	6 Fail	FALSE	TRUE	6.33	2.18			

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37754_at	LGALS3BP	L13210	4	Pass	3.25	1.50	4	Fail	FALSE	1.50	2.17	lectin, galactoside-binding, soluble, 3 binding protein (galactin 6 binding protein); LGALS3BP	17q25	
33387_at	GAS7	AB007854	4	Pass	6.00	1.83	5	Fail	FALSE	2.80	2.14	growth arrest-specific 7; GAS7	17p	
35960_at	IKBKB	AF031416	4	Pass	9.25	2.22	6	Fail	FALSE	4.33	2.13	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta; IKBKB	8p11.2	Kinase
40350_at	CT10RF13	M91083	5	Pass	19.20	4.09	4	Fail	FALSE	9.00	2.13	chromosome 11 open reading frame 13; CT10RF13	11p15.5	
1397_at	MAP3K11	L32976	4	Pass	4.25	1.50	3	Fail	FALSE	2.00	2.13	mitogen-activated protein kinase kinase kinase 11; MAP3K11	11q13.1-q13.3	Kinase
33528_at	KIAA0125	D50915	4	Pass	4.25	0.96	3	Fail	FALSE	2.00	2.13	KIAA0125 gene product; KIAA0125		
38995_at	CLDN5	AF000959	4	Pass	14.00	3.74	5	Fail	FALSE	6.60	2.12	claudin 5 (transmembrane protein deleted in velocardiofacial syndrome); CLDN5	22q11.21	
19891_at	UNK_A12	A1246730	4	Pass	12.00	3.56	6	Fail	FALSE	5.67	2.12	transcription factor binding to IGIM enhancer	Xp11.22	Kinase
34669_at	TFEB	X96717	5	Pass	6.00	1.22	6	Fail	FALSE	2.83	2.12	mitogen-activated protein kinase 3; MAPK3	16p11.2	Kinase
40925_at	UNK_AAS	AA55945	4	Pass	9.50	2.65	6	Fail	FALSE	4.50	2.11	aminomethyltransferase (glycine cleavage system p21.1)	3p21.2-p21.1	
1000_at	MAPK3	X60188	6	Pass	7.33	3.08	6	Fail	FALSE	3.50	2.10	kinase 3; MAPK3		
35763_at	UNK_ABG	AB011112	6	Pass	8.83	5.64	4	Fail	FALSE	4.25	2.08	KIAA0540 protein; KIAA0540		
41120_at	AMT	D14686	6	Pass	4.50	1.52	6	Fail	FALSE	2.17	2.08	protein T1; AMT		
703_at	UNK_L23	L23566	4	Pass	14.50	9.98	3	Fail	FALSE	7.00	2.07	oxidoreductase; POR	7q11.2	
858_at	POR	S90469	4	Pass	7.75	3.30	4	Fail	FALSE	3.75	2.07	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma; IKBKG		
1089_i at	UNK_M64	M64926	4	Pass	2.75	1.50	3	Fail	FALSE	1.33	2.06	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VII); integrin, alpha 5 (fibronectin receptor, alpha4q13)	12q11-q13	
36004_at	IKBKG	AF074382	4	Pass	15.75	3.86	3	Fail	FALSE	7.67	2.05	cystinosis, nephropathic; CTNS	17p13	
34868_at	KIAA1089	AB029012	5	Pass	4.60	1.14	4	Fail	FALSE	2.25	2.04	endoglin (Oster-Rendu-Weber syndrome D); ENG	9q33-q34.1	
36184_at	PLOD	L06419	5	Pass	11.00	8.60	5	Fail	FALSE	5.40	2.04	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VII); integrin, alpha 5 (fibronectin receptor, alpha4q13)	12q11-q13	
39753_at	ITGA5	X06256	4	Pass	9.50	4.65	3	Fail	FALSE	4.67	2.04	polypeptide; ITGA5	17p13	
36566_at	CTNS	AJ222967	4	Pass	4.00	1.41	1	Fail	FALSE	2.00	2.00	cystinosis, nephropathic; CTNS		
32562_at	ENG	X72012	4	Pass	8.00	2.71	3	Fail	FALSE	4.00	2.00	endoglin (Oster-Rendu-Weber syndrome D); ENG	9q33-q34.1	
4095_at	IL15RA	U31628	4	Pass	4.00	0.82	3	Fail	FALSE	2.00	2.00	interleukin 15 receptor, alpha; IL15RA	10p15-p14	
38020_at	KIAA0652	AB014552	5	Pass	4.80	2.39	5	Fail	FALSE	2.40	2.00	KIAA0652 gene product; KIAA0652	11	
40739_at	CA4	M83670	5	Pass	6.00	1.87	6	Fail	FALSE	3.00	2.00	carbonic anhydrase IV; CA4	17q23	
32802_at	TEB4	AB011169	6	Pass	8.67	4.50	6	Fail	FALSE	4.33	2.00	similar to S. cerevisiae SSN4; TEB4	5p15.2	

\*

Ally Qualifier	Ally Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of abs dec	Present in RA and Normal	Present in RA, Absent in Normal	Avg Freq (Normal)	Fold Change RA / Normal	Name	Chromosome	Kinase or Phosphatase
36307_at	KIAA0278	D87468	5	Pass	12.80	4.55	4 Fail	FALSE	TRUE	6.50	1.97	activity-regulated cytoskeleton-associated protein; ARC	8q24.3	
35230_at	CL24751	AF070530	5	Pass	8.80	3.03	6 Fail	FALSE	TRUE	4.50	1.96	hypothetical protein, clone 24751; CL24751	19	
35411_at	ATP-BL	AB018551	6	Pass	12.50	4.68	5 Fail	FALSE	TRUE	6.40	1.95	ATP synthase, subunit b-like; ATP-BL	16q24	
37098_at	PPOX	D38537	5	Pass	7.80	2.05	5 Fail	FALSE	TRUE	4.00	1.95	protoporphyrinogen oxidase; PPOX	1q22	
37149_s_at	UNK U95A	U95626	4	Pass	10.00	8.29	3 Fail	FALSE	TRUE	25.00	-2.50	lactotransferrin; LTF	#N/A	

qualifier	name	Accession	sum of abs dec	4 of 6 present	Avg Freq RA	Std Dev RA	sum of abs dec	Present in RA and Normal	Present in RA, Absent in Normal	Avg Freq (Normal)	Fold Change RA / Normal	Name	Chromosome
1029_s_at	UNK U07	U07794	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	FALSE	2.43	#DIV/0!	TXK tyrosine kinase; TXK	4p12
31495_at	SCYC2	D63789	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	TRUE	4.29	#DIV/0!	small inducible cytokine subfamily C, member 1 (lymphotactin); small inducible cytokine subfamily C, member 2; SCYC1, SCYC2	1q21-1q25, 1q23-1q25
32319_at	TNFSF4	AL022310	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	TRUE	10.00	#DIV/0!	tumor necrosis factor (ligand) superfamily, member 4 (tax-transcriptionally activated glycoprotein 1, 34KD); TNFSF4	1q25
32350_at	MALT1	AB026118	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	TRUE	2.43	#DIV/0!	mucosa associated lymphoid tissue lymphoma translocation gene 1; MALT1	18q21
32539_at	COP9	U51205	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	FALSE	5.29	#DIV/0!	COP9 homolog; COP9	
33410_at	ITGA6	S66213	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	TRUE	2.29	#DIV/0!	integrin alpha 6; ITGA6	2
34704_at	UNK_AA1	AA151971	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	TRUE	3.57	#DIV/0!	HERV-H LTR-associating 1; HHLA1	8q24
34875_at	KIAA0203	D86958	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	TRUE	2.57	#DIV/0!	KIAA0203 gene product; solute carrier family 22 (organic anion transporter), member 6; KYNENINASE (L-tryptophanase); KYN	8
36237_at	SLC22A6	AB009698	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	TRUE	3.14	#DIV/0!	KIAA0203 solute carrier family 22 (organic anion transporter), member 6; KYNENINASE (L-tryptophanase); KYN	11q11
38492_at	KYNU	D55639	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	TRUE	3.14	#DIV/0!	Kynureninase (L-tryptophanase); KYNU	
38512_at	ELAVL3	D26158	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	TRUE	22.71	#DIV/0!	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C3); ELAVL3	19p13.2
40590_at	CDC27	AA166687	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	TRUE	3.57	#DIV/0!	cell division cycle 27; CDC27	17q12-17q23.2
526_s_at	PMS2	U13696	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	TRUE	2.71	#DIV/0!	poonaesic segregation increased (S. cerevisiae) 2; PMS2	7p22
AFFX-M77833	28SRNAMC	M27830	0	Fail	#DIV/0!	#DIV/0!	7 Pass	FALSE	TRUE	39.14	#DIV/0!	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2; ELAVL2	9p21
36411_s_at	ELAVL2	U29943	0	Fail	#DIV/0!	#DIV/0!	8 Pass	FALSE	TRUE	7.25	#DIV/0!	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2; ELAVL2	

Atty Qualifier	Atty Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of abs present dec	Present in RA and Normal	Present in RA, Absent in Normal	Avg Freq RA, (Normal)	Fold Change RA / Normal	Name	Chromosome	Active or Phosphatase
38660_at	COX6A2	F27891	0	Fail	#DIV/0!	#DIV/0!	8 Pass	FALSE	FALSE	2.63	#DIV/0!	cytochrome c oxidase subunit VIa polypeptide 2; COX6A2	16p	
32641_at	KIAA0979	AB021196	0	Fail	#DIV/0!	#DIV/0!	9 Pass	FALSE	FALSE	2.56	#DIV/0!	KIAA0979 protein, androgen-induced prostate proliferative shut-off associated protein; AS3.KIAA0979	13q12-q13.13q12.3	
32941_at	ICSBP1	M69196	0	Fail	#DIV/0!	#DIV/0!	9 Pass	FALSE	FALSE	8.22	#DIV/0!	interferon consensus sequence binding protein 1; ICSBP1		
148_at	ELL2	U88629	1	Fail	11.00	#DIV/0!	7 Pass	FALSE	FALSE	3.71	2.96	ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR; ELL2		
35590_s_at	GPR	X81832	3	Fail	25.33	2.89	7 Pass	FALSE	FALSE	9.43	2.69	gastric inhibitory polypeptide receptor; GPR	19q13.3	
31559_at	SLC13A2	U26209	3	Fail	11.67	2.08	7 Pass	FALSE	FALSE	4.43	2.43	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2; SLC13A2	17p11.1-q11.1	
34903_at	UNK_A10	A1017382	3	Fail	15.67	7.09	9 Pass	FALSE	FALSE	6.22	2.52	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 (39kD); NDUFA9	12p13.3	
36205_at	NDUFA9	L04490	1	Fail	11.00	#DIV/0!	7 Pass	FALSE	FALSE	4.43	2.48			
32048_at	UNK_A10	AL049675	3	Fail	11.33	3.79	8 Pass	FALSE	FALSE	4.63	2.45	nucleolar cysteine-rich protein; HSA(659)		
37521_s_at	HSA6591	H82458	1	Fail	10.00	#DIV/0!	7 Pass	FALSE	FALSE	4.14	2.41			
396_f_at	EPOR	X97671	2	Fail	29.50	0.71	9 Pass	FALSE	FALSE	12.44	2.37	erythropoietin receptor; EPOR	19p13.3-p13.2	
34098_f_at	UNK_A17	A199757	2	Fail	7.50	2.12	7 Pass	FALSE	FALSE	3.29	2.28	keratin, hair, acidic, 3A; KRTHA3A	17q12-q21	
31594_at	KRTHA3A	Y16788	2	Fail	11.00	5.66	7 Pass	FALSE	FALSE	4.86	2.26	coricotrophin releasing hormone receptor 1; CRHR1	17q12-q22	
40651_s_at	CRHR1	AF039523	1	Fail	7.00	#DIV/0!	10 Pass	FALSE	FALSE	3.10	2.26			
40299_at	REZ	AF091890	2	Fail	35.50	13.44	8 Pass	FALSE	FALSE	15.75	2.25	G-protein coupled receptor; REZ		
33037_at	UNK_A10	AL022165	1	Fail	7.00	#DIV/0!	8 Pass	FALSE	FALSE	3.13	2.24	chondroitin 6-sulfotransferase-2; C6ST-2	Xp11	
30920_r_at	CRF	AF095154	3	Fail	93.33	14.05	10 Pass	FALSE	FALSE	41.70	2.24	CRF-related factor; CRF	17q21	
31586_f_at	UNK_X72	X72475	3	Fail	8.67	2.89	9 Pass	FALSE	FALSE	3.89	2.23			
37488_at	FNTB	L00635	2	Fail	7.00	1.41	7 Pass	FALSE	FALSE	3.14	2.23	farnesyltransferase, CAA-X box, beta; FNTB	4q23-q24	
2047_s_at	JUP	M23410	3	Fail	17.33	9.29	8 Pass	FALSE	FALSE	7.88	2.20	junction plakoglobin; JUP	12q21	
1888_s_at	GDF1	M62302	3	Fail	10.33	0.58	8 Pass	FALSE	FALSE	4.75	2.18	growth differentiation factor 1; GDF1	19p12	
40622_r_at	UNK_A10	AL096740	3	Fail	38.00	13.11	9 Pass	FALSE	FALSE	17.56	2.16			
41324_g_at	FOXN1	U90917	1	Fail	16.00	#DIV/0!	10 Pass	FALSE	FALSE	7.50	2.13	forkhead box M1; FOXM1	12p13	
39844_at	UNK_A18	A1806379	2	Fail	8.00	2.83	12 Pass	FALSE	FALSE	3.83	2.09			
34815_at	TNRC12	U80743	1	Fail	5.00	#DIV/0!	7 Pass	FALSE	FALSE	2.43	2.06	truncal repeat containing L2; TNRC12	12qter	
33493_at	HPL-EDD4	AF048849	2	Fail	10.00	2.83	8 Pass	FALSE	FALSE	4.88	2.05	erythroid differentiation and demucification factor 1; HPL-EDD4		
1581_s_at	UNK_M27	M27504	1	Fail	5.00	#DIV/0!	9 Pass	FALSE	FALSE	2.44	2.05	topoisomerase (DNA) II beta (180kD); TOP2B	3p24	
33697_at	P2RX7	Y12851	3	Fail	7.00	1.00	8 Pass	FALSE	FALSE	3.50	2.00	purinergic receptor P2X, ligand-gated ion channel, 7; P2RX7	12q24	
31503_at	UNK_W28	W28732	2	Fail	9.50	7.78	11 Pass	FALSE	FALSE	4.82	1.97			

HuBMC\_RA\_U95A-Kin-PhosP.xls

Affy Qualifier	Affy Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of abs dec	Present in RA and Normal	Present in RA, Absent in Normal	Avg Freq (Normal)	Change RA / Normal	Name	Chromosome	kinase or Phosphatase
718_at	PRSS11	D87258	2	Fail	4.50	0.71	7 Pass	FALSE	FALSE	2.29	1.97	protease, serine, 11 (IGF binding); PRSS11	10q25.3-q26.2	
38229_at	UNK_X90	X90579	3	Fail	92.33	20.98	7 Pass	FALSE	FALSE	47.00	1.96			
393_x_at	RUNX1	X90976	2	Fail	5.00	0.00	11 Pass	FALSE	FALSE	2.55	1.96	run-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene); RUNX1	21q22.3	
1170_at	CSF1	M37435	1	Fail	9.00	#DIV/0!	10 Pass	FALSE	FALSE	4.60	1.96			
40490_at	DDX21	U41387	3	Fail	3.67	1.53	11 Pass	FALSE	FALSE	7.82	-2.13	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 21; DDX21	#N/A	

CIA PRMC data Fold changes are shown as normalized

TBS= total body score

TBS-7-

TBS 0* Systematic	Preart										Common	Genbank	EC	Description	Phenotype	Map	Keywords	Symbol
	Control	hrtic	TBS-1	TBS-2	TBS-3	TBS-4	TBS-5	TBS-6	9									
J03023	0	-1.62	1.08	-3.25	2.23	1.54	1.54	1.62		hemopoietic cell kinase; Hck	J03023	2.7.1.112	TYROSINE- PROTEIN KINASE HCK (EC 2.7.1.112) AND P60- HCK) (HEMOPOIET IC CELL KINASE) (B- CELL/MYELO ID KINASE)	EXPRESSED PREDOMINA NTLY IN CELLS OF THE MYELOID AND B- LYMPHOID LINEAGES.	286.0 cM	Hemostasis	Hck	
AA028657	0	3.00	19.00	17.00	17.00	37.50	16.50	20.00		EST; Unknown	AA028657						EST; Unknown	Unknown
Msa.10146.0	0	1.80	12.40	13.80	13.60	19.60	15.20	19.20		vWF, human	AA168633						Hemostasis	
Msa.10146.0	0	1.80	12.40	13.80	13.60	19.60	15.20	19.20		vWF, human	AA168633						Hemostasis	
W62701	0	2.40	20.20	19.00	16.40	22.80	18.20	18.80			W62701							
W62701	0	2.40	20.20	19.00	16.40	22.80	18.20	18.80			W62701							
Msa.1497.0	0	1.50	7.00	5.50	6.00	11.00	6.50	15.50		calmodulin 3; Calm3	M19380	2.7.1.38				74.0 cM	Regulatory	Calm3
Msa.1497.0	0	1.50	7.00	5.50	6.00	11.00	6.50	15.50		calmodulin 3; Calm3	M19380	2.7.1.38				74.0 cM	Regulatory	Calm3
Msa.723.0	0	2.00	8.00	5.00	3.00	10.00	9.00	15.00		aquaporin 1; Aqp1	L02914		AQUAPORIN- CHIP (WATER CHANNEL PROTEIN FOR RED BLOOD CELLS AND KIDNEY PROXIMAL TUBULE) (AQUAPORIN 1) (EARLY RESPONSE	ERYTHROCY TES AND RENAL TUBULES.	627.0 cM	Cell Surface Protein	Aqp1	
D16262	0	0.00	9.00	10.00	8.00	21.00	16.00	14.00		mesoderm specific transcript; Mest	D16262					67.5 cM	Cytokine	Mest



# Table 2001

X15592	0	1.33	13.67	13.00	16.67	14.67	13.00	14.00	cytotoxic T lymphocyte-associated protein 2 beta; Ctla2b	X15592		CTLA-2-BETA PROTEIN PRECURSOR (FRAGMENT)		13 42.0 cM		Ctla2b
Msa.3237.0	0	0.00	7.50	9.00	9.00	9.50	9.50	13.50	four and a half LIM domains 1; Fhl1	W14830			X A6-A7.1	Regulatory	Fhl1	
M87276	0	0.00	6.00	7.00	5.00	10.00	11.00	13.00	thrombospondin 1; Thbs1	M87276		THROMBOSPONDIN 1 PRECURSOR		2 65.0 cM	Extracellular Protein	Thbs1
AA616664	0	0.00	10.75	11.00	10.00	16.75	12.00	11.25		AA616664						
W45778	0	1.27	8.47	9.40	9.00	9.53	8.00	9.27	von Willebrand Factor; vWF; homolog	W45778					Hemostasis	vWF
W64688	0	0.00	6.82	7.36	5.55	9.82	7.09	8.73		W64688					EST; Unknown	
ab000822	0	1.10	7.30	7.10	7.80	10.10	7.70	8.50	synaptosomal-associated protein, 23kD; Snap23	AB000822				2 61.8 cM		Snap23
M19380	0	0.00	4.67	4.00	5.33	9.00	6.67	8.33	calmodulin 3; Calm3	M19380	2.7.1.38			7 4.0 cM	Regulatory	Calm3
AA542220	0	-1.09	5.00	4.75	7.00	8.92	5.92	7.50	TBX1 protein; TBX1	AA542220		TBX1 PROTEIN (T-BOX PROTEIN 1) (TESTIS-SPECIFIC T-BOX	TESTIS SPECIFIC		Intracellular Protein	TBX1
Msa.1160.0	0	0.00	7.67	2.00	7.67	2.00	5.33	5.67	serum amyloid A 3; Saa3	X03505		SERUM AMYLOID A-3 PROTEIN PRECURSOR	FOUND IN VARIOUS TISSUES	7 23.5 cM	Extracellular Protein	Saa3
X03479	0	-1.20	6.17	1.50	5.17	1.67	3.50	5.17	serum amyloid A 3; Saa3	X03479		SERUM AMYLOID A-3 PROTEIN PRECURSOR	FOUND IN VARIOUS TISSUES	7 23.5 cM	Extracellular Protein	Saa3
U92478	0	0.00	3.00	2.33	3.33	6.00	5.33	4.67	development and differentiation enhancing; Ddef1	U92478					Regulatory	Ddef1

# Table 1

Msa.3665.0	0	-1.12	3.33	4.00	3.67	5.44	4.67	4.67	DNA segment, Chr 2, Wayne State University 143, expressed; D2Wsu143c	AA116604					2 24.0 cM	Proteolytic	D2Wsu143c
D67016	0	-2.33	-1.75	-1.75	1.14	3.14	1.14	4.43	heat shock protein, 105 kDa; Hsp105	D67016			HEAT-SHOCK PROTEIN 105 KDA (HEAT SHOCK- RELATED 100 EXPRESSED KDA PROTEIN E7I) (HSP-E7I) (HEAT SHOCK 110 KDA PROTEIN) (42)	FOUND IN MOST TISSUES. HIGHLY EXPRESSED IN BRAIN.	5 88.0 cM		Hsp105
AA120653	0	-1.69	2.84	2.41	2.77	4.50	3.07	3.80	transgelin 2; Tagln2	AA120653					1 94.2 cM	Structural Protein	Tagln2
AA285502	0	-2.00	2.00	2.00	2.00	4.50	3.50	3.75	receptor (calctonin) activity modifying protein 1; Ramp1	AA285502						Regulatory	Ramp1
U35124	0	-1.87	2.07	2.00	2.27	4.00	2.73	3.67	protein tyrosine phosphatase, non-receptor type 18; Ptpn18	U35124					1 17.3 cM	Regulatory	Ptpn18
U05837	0	-1.60	0.00	-1.14	1.75	2.25	2.00	3.50	hexosaminidase A; Hexa	U05837	3.2.1.52		BETA- HEXOSAMINI DASE ALPHA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL- BETA- GLUCOSAMI NIDASE) (BETA-N- ACETYLHEX OSAMINIDAS E)		9 29.0 cM	Proteolytic	Hexa



# Table 1

X15591	0	1.03	3.05	2.89	3.02	1.95	2.10	2.63	cytotoxic T lymphocyte-associated protein 2 alpha; C12a2a	X15591		CTLA-2-ALPHA PROTEIN PRECURSOR.	13 36.0 cM	Cell Surface Protein	C12a2a
U88328	0	-1.33	1.88	1.50	4.88	2.38	1.50	2.63	cytokine inducible SH2-containing protein 3; C12a3	U88328		CYTOKINE INDUCIBLE SH2-CONTAINING PROTEIN 3 (PROTEIN EF-10).		ECM (Matrix Prot)	C12a3
Msa.4067.0	0	-1.25	1.20	1.80	3.20	2.40	1.20	2.60	Sip1?	AA003876				Unknown	
AA289661	0	-1.75	1.90	2.05	3.86	3.76	2.00	2.57	EST; Unknown	AA289661				EST; Unknown	Unknown
AF003693	0	-1.39	2.56	2.00	3.36	3.64	2.92	2.56	syndecan binding protein; Sdcbp	AF003693					Sdcbp
AA184116	0	-2.00	2.50	3.00	4.30	3.80	3.20	2.50	homolog of Alpha-actinin (human)	AA184116				Structural Protein	
U71205	0	0.00	3.00	3.00	4.00	5.50	3.00	2.50	RAS-like protein expressed in many tissues; Rit	U71205				Transcription Factor	Rit
Msa.36175.0	0	-1.33	2.50	2.50	16.00	2.50	2.25	2.50		AA124453				EST; Unknown	
Msa.22134.0	0	0.00	1.50	0.00	7.50	1.50	1.50	2.50	Unknown	AA031158				EST; Unknown	
X56602	0	0.00	8.50	1.50	1.50	0.00	1.50	2.50	interferon-stimulated protein (15 kDa); Isg15	X56602		UBIQUITIN CROSS-REACTIVE PROTEIN (INTERFERON-N-STIMULATE)		Cytokine	Isg15
U19118	0	-2.00	-1.33	-4.00	-1.33	0.00	1.50	2.50	activating transcription factor 3; AIF3	U19118		CYCLIC-AMP-DEPENDENT TRANSCRIPT ION FACTOR AIF-3 (ACTIVATING TRANSCRIPT ION FACTOR 3) (TRANSCRIP			AIF3

# Table 200

AA123934	0	-2.67	-2.00	-4.00	0.00	1.38	1.25	2.38	EST; Unknown	AA123934						EST; Unknown	Unknown
L28177	0	-1.20	2.17	2.33	4.50	2.83	2.67	2.33	DNA-damage inducible transcript 1; Ddit1; (GADD45a)	L28177				GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN	3 70.5 cM	Intracellular Protein	Ddit1
Msa.641.0	0	-1.49	2.11	1.91	3.47	2.27	1.92	2.31	Fc receptor, IgE, high affinity I, gamma polypeptide; Fcε1g	W41745				HIGH AFFINITY IMMUNOGLOBULIN RECEPTOR GAMMA-SUBUNIT PRECURSOR (FCER1) (IGE FC RECEPTOR, GAMMA-SUBUNIT)	1 93.3 cM	Receptor	Fcε1g
AA033074	0	-1.43	2.30	1.40	3.10	3.10	1.70	2.30	flotillin 1; Flot1	AA033074							Flot1
U73004	0	-1.14	1.91	2.18	3.48	3.06	2.27	2.15	secretory leukocyte protease inhibitor; Slpi	U73004				ANTILEUKOPROTEINASE 1 PRECURSOR (ALP) (SECRETORY INTESTINE LEUKOCYTE AND PROTEASE INHIBITOR).	HIGHEST EXPRESSION IN LUNG, SPLEEN, (SECRETORY INTESTINE AND EPIDIDYMIS WITH LOWER LEVELS IN LIVER AND SEMINAL VESICLE. NO EXPRESSION IN BRAIN, HEART, KIDNEY AND	Proteolytic	Slpi

D37837	0	-1.20	0.00	-1.29	3.39	1.28	1.39	2.06	plasmin 2, L; Pls2	D37837		L-PLASTIN (LYMPHO- CYTOSOLIC PROTEIN 1) (LCP-1) (65 KDA MACROPHAGE PROTEIN)				Pls2
X81627	0	1.43	4.86	3.14	17.29	3.14	2.14	2.00	lipocalin 2; Lcn2	X81627		NEUTROPHIL GELATINASE- ASSOCIATED LIPOCALIN PRECURSOR (NGAL) (P25) (SV-40 INDUCED 24P3		2.27.0 cM	Extracellular Protein	Lcn2
Msa.2129.0	0	2.00	6.33	3.67	31.67	3.33	2.00	2.00	lipocalin 2; Lcn2	W13166		NEUTROPHIL GELATINASE- ASSOCIATED LIPOCALIN PRECURSOR (NGAL) (P25) (SV-40 INDUCED 24P3		2.27.0 cM	Extracellular Protein	Lcn2
U96687	0	0.00	1.47	-1.25	3.07	1.73	1.53	2.00	paired-Ig-like receptor A10,paired-Ig- like receptor A6; Pira10,Pira6	U96687						Pira10,Pira6
U27838	0	-3.50	-1.40	-3.50	0.00	1.57	1.29	2.00	GPI-anchored membrane protein I; Gpiap-pending	U27838						Gpiap-pending
Msa.3234.0	0	-1.33	-2.00	-4.00	2.75	1.25	0.00	2.00	myosin II; MyoIf	X97650						MyoIf
AA032906	0	-9.00	-9.00	-9.00	-4.50	-1.50	-1.29	2.00	Homologous to GENESEQN:V 49566 (human)	AA032906						Patented; Novel
AA032906	0	-9.00	-9.00	-9.00	-4.50	-1.50	-1.29	2.00	Homologous to GENESEQN:V 49566 (human)	AA032906						Patented; Novel

# Table 1

AA271024	0	-4.00	-4.00	-6.00	-1.33	1.08	-1.09	1.92	small nuclear ribonucleoprotein D2 polypeptide (SNRPD2)	AA271024					Other	
Msa.31660.0	0	-1.58	1.37	1.07	3.07	1.20	1.53	1.87	CD53 antigen, Cd53	AA105582				LEUKOCYTE SURFACE ANTIGEN CD53 (CELL SURFACE GLYCOPROTEIN CD53).	Cell Surface Protein	Cd53
ET62056	0	-3.22	-1.76	-2.32	1.45	1.29	1.33	1.86	immunoglobulin rearranged kappa chain	ET62056					Extracellular Protein	
ab009287	0	-2.33	-3.50	-7.00	0.00	1.14	0.00	1.86	CD68 antigen, Cd68	AB009287				EXPRESSED IN TISSUE MACROPHAGES AND TO A LESSER EXTENT IN DENDRITIC CELLS.	Cell Surface Protein	Cd68
AA241085	0	-4.00	1.17	1.08	1.42	2.08	1.67	1.83	GENESEQN:Z 34468 Mouse 15 kDa selenoprotein	AA241085						
AA020104	0	-3.25	-1.62	-1.30	1.23	1.62	1.23	1.77	glycosylation dependent cell adhesion molecule 1; Glycam1	AA020104				SULFATED 50 KDA GLYCOPROTEIN PRECURSOR (SGP50) (ENDOTHELIAL LIGAND FOR L-SELECTIN) (GLYCOSYLATION-DEPENDENT CELL ADHESION MOLECULE)		Glycam1
Msa.38664.0	0	-2.13	-1.06	-1.89	4.88	1.12	1.06	1.76		AA144469					EST; Unknown	

# Table 1: Cathepsins

X94353	0	-1.33	3.00	2.25	5.50	1.75	1.75	1.75	1.75	cathepsin-like protein, Cnlp	X94353		CATHEPSIN-RELATED ANTIMICROBIAL PEPTIDE STOMACH, PRECURSOR AND (CRAMP) (CATHEPSIN-LIKE PROTEIN) (CLP).	EXPRESSED IN TESTIS, SPLEEN, STOMACH, AND INTESTINE. VERY LOW EXPRESSION FOUND IN HEART, LUNG AND SKELETAL MUSCLE. NO EXPRESSION IN BRAIN, KIDNEY OR LIVER.	9 61.0 cM	Metabolic	Cnlp
ET62844	0	-1.33	1.25	-1.33	3.13	1.75	1.38			paired-Ig-like receptor A10, paired-Ig-like receptor A6;	ET62844					7 Receptor	Pira10, Pira6
U06119	0	-2.88	-1.64	-3.29	1.17	1.35	1.26			cathepsin H; Cish	U06119	3 4.22.16	CATHEPSIN H PRECURSOR (EC 3.4.22.16) (CATHEPSIN B3) (CATHEPSIN BA).	WIDELY EXPRESSED WITH HIGHEST EXPRESSION FOUND IN NON-SKELETAL TISSUES. LOW LEVELS FOUND IN SKELETAL TISSUE.	9 50.0 cM	Proteolytic	Cish
M35153	0	-1.75	1.29	1.29	3.71	1.71	2.00			lamin B1; Lmnb1	M35153		LAMIN B1.		18 29.0 cM	ECM (Matrix Prot)	Lmnb1
Msa.739.0	0	-1.04	2.08	1.17	5.63	1.79	1.33			haptoglobin; Hfp	M96827				8 55.0 cM	Extracellular Protein	Hfp
AA445408	0	-5.00	-2.50	-10.00	-1.43	-1.43	1.20			H3 histone, family 3B; H3f3b	AA445408						H3f3b



# Table 1

Msa.7498.0	0	-1.50	1.67	1.33	0.00	3.67	1.33		1.67	growth arrest and DNA-damage-inducible, gamma; Gadd45g	AA138777	GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD45 GAMMA (CYTOKINE RESPONSIVE)			Regulatory	Gadd45g
Msa.1903.0	0	-3.63	-2.07	-4.83	-1.61	1.03	-1.38	1.66	1.66	histocompatibility 2, class II, locus Dma,histocompatibility 2, class II, locus Mb1,histocompatibility 2, class II, locus Mb2,proteosome (prosome, macropain) subunit, beta type 9 (large multifunctional protease 2); H2-Dma,H2-DMb1,H2-DMb2,Pmb9	U35323	CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECURSOR, CLASS II HISTOCOMPATIBILITY ANTIGEN, M BETA 1 CHAIN PRECURSOR (H2-M BETA 1 CHAIN),PRO TEASOME CHAIN 7 PRECURSOR (EC 3.4.99.46) (MACROPAIN CHAIN 7) (MULTICATALYTIC ENDOPEPTIDASE	17 18.56 cM,17 18.57 cM,17 18.58 cM,17 18.59 cM	□	H2-DMa,H2-DMb1,H2-DMb2,Pmb9	
U96689	0	-1.06	1.59	1.29	1.94	3.18	1.65	1.65	1.65	paired-Ig-like receptor B; Pirb	U96689			7 1.0 cM	Receptor	Pirb
V01527	0	-3.55	-1.95	-4.33	-1.30	0.00	-1.11	1.62	1.62	histocompatibility 2, class II antigen A, beta 1; H2-Ab1	V01527	H-2 CLASS II HISTOCOMPATIBILITY ANTIGEN, A-D BETA CHAIN	17 18.64 cM	Cell Surface Protein	H2-Ab1	
AA285691	0	-3.29	-1.55	-2.32	1.37	1.37	1.01	1.61	1.61	cytohesin binding protein (Cbp)	AA285691				Cell Surface Protein	

# Table 1

XS1829	0	-5.00	-2.50	-3.33	-1.25	-1.25	-1.11	1.60	myeloid differentiation primary response gene 116; Myd116	XS1829	MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116				Other	Myd116
AA185060	0	-3.50	-2.33	-2.33	0.00	1.29	0.00	1.57	GENESEQ:Z 52941 Human prostate tumor cDNA library derived EST fragment #84	AA185060					Unknown	
US9488	0	-1.75	-2.33	-3.50	1.43	-1.17	0.00	1.57	neutrophil cytosolic factor 4; Ncf4	US9488	NEUTROPHIL CYTOSOL FACTOR 4 (NCF-4)		15 47.2 cM		Intracellular Protein	Ncf4
L37297	0	-2.00	3.00	2.00	20.75	2.50	2.00	1.50	neutrophilic granule protein; Ngp	L37297					Intracellular Protein	Ngp
L37297	0	-2.00	3.00	2.00	20.75	2.50	2.00	1.50	neutrophilic granule protein; Ngp	L37297					Intracellular Protein	Ngp
D73368	0	-4.00	-3.00	-6.00	-1.20	1.08	0.00	1.50	enhancer of rudimentary homolog (Drosophila); Erh	D73368	DEAD-BOX PROTEIN 3 (DEAD-BOX RNA HELICASE DEAD3) (EMBRONIC RNA HELICASE) (DIPAS1) RELATED	DEVELOPMENTALLY REGULATED			Other	Erh
K01923	0	-3.75	-1.54	-2.92	-1.14	1.04	1.03	1.50	histocompatibility 2, class II antigen A, alpha; H2-Aa	K01923	H-2 CLASS II HISTOCOMPATIBILITY ANTIGEN, A-K ALPHA CHAIN		17 18.65 cM		Cell Surface Protein	H2-Aa

# Protein Data Bank

Msa.1700.0	0	-1.37	1.36	1.32	1.09	1.45	phospholipase A2 group VII (platelet-activating factor acetylhydrolase, plasma); Pla2g7	U34277	3.1.1.47	PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47) (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE ESTERASE) (1-ALKYL-2-ACETYLGlycerophosphoCHOLINE	PLASMA	Cytokine	Pla2g7
C76739	0	-1.29	1.33	2.11	1.78	1.44	macrophage C-type lectin; Mpel	C76739				Cell Surface Protein	Mpel
U29947	0	-2.29	-1.78	1.19	1.13	1.44	mannosidase 2, alpha B1; Man2b1	U29947				Regulatory	Man2b1

\*

AA008321	0	-1.75	-1.75	-3.50	1.43	1.86	0.00	1.43	proteasome (prosome, macropain) subunit, alpha type 4; Psm4	AA008321	3.4.99.46	PROTEASOM E COMPONENT C9 (EC 3.4.99.46) (MACROPAIN SUBUNIT C9) (MULTICATALYTIC ENDOPEPTIDASE)			Proteolytic	Psm4
T25659	0	-3.50	-1.40	-2.33	1.14	1.14	0.00	1.43	heterogeneous nuclear ribonucleoprotein A2/B1; Hnrp2b1	T25659		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS A2/B1 (HNRNP A2)			EST; Unknown	Hnrp2b1
AA638408	0	-3.40	-2.83	-4.25	-1.42	-1.31	-1.13	1.41	arginine N-methyltransferase 1; Mm1	AA638408					Signal Transduction	Mm1
AA408475	0	-3.33	-2.50	-2.50	-1.11	1.50	1.30	1.40	ribosomal protein L13a; Rpl13a	AA408475		60S RIBOSOMAL PROTEIN L13A (TRANSLATION ANTIGEN PI98) (TUM-PI98)	7 25.0 cM		Intracellular Protein	Rpl13a
M59378	0	-3.25	-1.86	-3.25	-1.18	1.08	-1.30	1.38	tumor necrosis factor receptor superfamily, member 1b; Tnfrsf1b	M59378		TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75)	4 75.5 cM		Receptor	Tnfrsf1b
AA189914	0	-1.26	2.08	2.83	2.79	3.92	2.38	1.38	cytidine monophosphate N-acetylneuraminic acid synthetase; Cmas	AA189914			6 74.0 cM			Cmas
AA261402	0	-2.78	-1.92	-3.57	1.04	1.24	-1.14	1.36	EST; Unknown	AA261402					EST; Unknown	Unknown

\*

# Table 1. The root

AA174982	0	-2.37	-1.76	-3.10	1.17	1.11	-1.17	1.36	coronin, actin binding protein 1A; Corolla	AA174982			CORONIN-LIKE PROTEIN P57 (CORONIN 1A)		7 62.5 cM	Intracellular Protein	Corolla
AA182228	0	-2.56	-3.29	-7.67	-1.15	-1.21	-1.28	1.35	EST; Unknown	AA182228						EST; Unknown	Unknown
AF032466	0	-1.50	2.33	1.67	6.00	2.33	1.33	1.33	arginase type II; Arg2	AF032466	3.5.3.1		ARGINASE II PRECURSOR (EC 3.5.3.1) (NON-HEPATIC ARGINASE) (KIDNEY-TYPE)				Arg2
AA152590	0	-3.00	-2.25	-4.50	-1.29	1.44	1.11	1.33	eukaryotic translation initiation factor 4A1; Eif4a1	AA152590					11 39.0 cM	Translation Factor	Eif4a1
AA273932	0	-3.57	-2.08	-2.78	-1.19	1.08	-1.09	1.32	aldo-keto reductase; LOC56043	AA273932						Other	LOC56043
AA189758	0	-3.25	-1.86	-3.25	-1.18	1.08	1.15	1.31	Wbser5 gene product; Wbser5	AA189758						Regulatory	Wbser5
Msa.4530.0	0	-2.88	-1.92	-3.83	0.00	-1.15	-1.15	1.30	EST; region of homology to GENESEQN:Z 77537 Human ovarian tumor cDNA library derived EST fragment 88	AA106931						EST; Unknown	
K01925	0	-3.84	-1.66	-3.31	-1.16	-1.10	-1.10	1.30	histocompatibility 2, class II antigen A, alpha; H2-Aa	K01925			H-2 CLASS II HISTOCOMPATIBILITY ANTIGEN, A-K ALPHA CHAIN		17 18.65 cM	Hemostasis	H2-Aa

# Table 1

D10911	0	-1.27	1.93	1.57	4.50	2.00	1.64	1.29	a disintegrin and metalloproteas e domain (ADAM) 8; Adam8	D10911	3.4.24.-	ADAM 8 PRECURSOR (EC 3.4.24.-) (A DISINTEGRIN AND METALLOPR OTEINASE DOMAIN 8) (CELL SURFACE ANTIGEN MS2) (MACROPHA GE CYSTEINE- RICH	MACROPHAG7 F3-F5 ES.	Proteolytic	Adam8
M59821	#####	-3.15	-5.13	-5.86	-1.58	-1.78	-1.58	1.27	immediate early response 2, ler2	M59821		T- LYMPHOCYT E ACTIVATED PROTEIN (CYCLOHEXI MIDE- INDUCED) (CHX1) (IMMEDIATE EARLY		Intracellular Protein	ler2
AA575696	0	-3.00	-3.00	-4.00	1.33	1.17	1.08	1.25	sorting nexin 1; Snx1	AA575696				Regulatory	Snx1
AA575696	0	-3.00	-3.00	-4.00	1.33	1.17	1.08	1.25	sorting nexin 1; Snx1	AA575696				Regulatory	Snx1
AA172851	0	-1.26	2.24	1.66	5.66	2.17	1.41	1.21	EST; Unknown	AA172851				EST; Unknown	Unknown
AA285635	0	-3.00	-2.40	-6.00	-1.33	1.17	-1.71	1.17	ectoplacental cone, invasive trophoblast giant cells, extraembryonic ectoderm and chorion sequence 21; Eps21 - pending	AA285635				EST; Unknown	Eps21- pending
AA254740	0	-3.75	-1.67	-2.50	-1.15	1.13	0.00	1.13	Nop10p (human)	AA254740				Other	

Msa.928.0	0	-1.60	1.38	0.00	3.50	1.38	1.13	1.13	1.13	myristoylated alanine rich protein kinase C substrate; Macs	M60474	MYRISTOYL ATED ALANINE- RICH C- KINASE SUBSTRATE (MARCKS).	BRAIN, SPLEEN, LESS IN KIDNEY AND HEART, AND VERY LOW LEVELS IN	10 22.0 cM	Structural Protein	Macs
AA020128	0	-4.50	-3.00	-3.00	1.33	1.44	1.11	1.11	1.11	clathrin, light polypeptide (Lca); Clia	AA020128	CLATHRIN LIGHT CHAIN A.			Structural Protein	Clia
U91848	0	-5.00	-2.22	-4.00	-1.43	-1.33	0.00	1.10	1.10		U91848					
U16985	0	-3.12	-3.00	-4.26	-1.19	-1.09	-1.31	1.05	1.05	lymphotoxin B; Lib	U16985	LYMPHOTOX IN-BETA (LT- BETA) (TUMOR NECROSIS FACTOR C).		17 19.06 cM	Cytokine	Lib
Z27231	0	-1.17	2.00	0.00	5.86	1.71	1.29	0.00	0.00	matrix metalloprotein ase 9; Mmp9	Z27231	3.4.24.35  92 KDA TYPE IV COLLAGENA SE PRECURSOR (EC 3.4.24.35) (92 KDA GELATINASE (MATRIX ) METALLOPR OTEINASE-9) (MMP-9) (GELATINASE)		2 96.0 cM	Metabolic	Mmp9
D17630	0	-1.20	1.83	0.00	4.50	1.83	1.33	-1.20	-1.20	chemokine (C- X-C) receptor 2; Cmkar2	D17630	HIGH AFFINITY INTERLEUKI N-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA)		1 40.0 cM		Cmkar2





## Table 5

CIA-001,011,012pawsU-FC Raw data from GEDS Fold Change, Genes were originally filtered for Present/Absent using frequency data

Note here

Note here

Score (0\*

Systematic	control		prearth Score 1		Score 2		Score 3		Score 4	
	Raw	P	Raw	StdErr	Raw	StdErr	Raw	StdErr	Raw	StdErr
D37801	1.00	-1.13	-2.72	0.68	-1.99	0.15	-2.79	0.82	-2.51	0.14
AA204199	1.00	2.86	-3.91	2.24	-0.03	1.37	-2.26	0.12	-2.68	0.30
U28244	1.00	-1.70	-1.41	1.43	-0.79	1.88	-6.34	2.53	-6.56	1.87
Msa.30443.0	1.00	1.21	2.19	0.78	2.28	0.60	9.18	1.92	11.29	3.33

Common	Genbank	description	function	Map	Keywords	Kinase or Phosphatase
protein tyrosine phosphatase, non-receptor type 21; Ptpn21	D37801	protein tyrosine phosphatase, non-receptor type 21 (cc 3.1.3.48) (protein-tyrosine phosphatase ptp-rlid)	may be involved in the regulation of growth and differentiation of liver cells.			Phosphatase
protein tyrosine phosphatase 4a3; Ptp4a3	AA204199		northern blot analysis revealed that pti-2 is preferentially expressed in skeletal muscle, while pti-3 is preferentially expressed in both skeletal muscle and heart, although both pti-2 and pti-3 are expressed at lower levels in other tissues		Signal Transduction	Phosphatase
phospholipase A2, group IIA (platelets, synovial fluid); Pla2g2a	U28244	phospholipase a2, membrane associated precursor (cc 3.1.1.4) (phosphatidylcholine 2-acylhydrolase) (group ii phospholipase a2) (enhancing factor) (cd)	pa2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides.	4 68.0 cM		Phosphatase
RAS-related C3 botulinum substrate 2; Rac2	AA097231	ras-related c3 botulinum toxin substrate 2 (p21-rac2) (en-7 protein)	function: seems to be involved in the regulation of the nadph oxidase. subcellular location: cytoplasmic; membrane-associated when activated. tissue specificity: hematopoietic cells. similarity: homologous to the mouse		Intracellular Protein	Kinase

# Topical Estrogen

J03023	1.00	-1.22	0.45	0.71	0.96	2.17	3.77	0.26	4.24	0.44	hemopoietic cell kinase; Hck	J03023	tyrosine-protein kinase hck (ec 2.7.1.112) (p56-hck and p60-hck) (hemopoietic cell kinase) (b- cell/myeloid kinase) (bmk).	may serve as part of a signaling pathway coupling the fc receptor to the activation of the respiratory burst. may also contribute to neutrophil migration and may regulate the degranulation process of neutrophils.	286.0 cM	Hemostasis	Kinase	*
X06368	1.00	-2.02	-2.80	1.36	-0.30	1.81	1.50	0.23	1.45	0.19	colony stimulating factor 1 receptor; Csf1r	X06368	macrophage colony stimulating factor 1 receptor precursor (csf-1-r) (ec 2.7.1.112) (fms proto-oncogene) (c- fms)	this protein is the receptor for csf-1, it is a protein tyrosine- kinase transmembrane receptor.	1830.0 cM	Cytokine	Kinase	*
Msa.1709.0	1.00	-1.81	-3.77	0.76	-1.37	2.51	-1.58	0.33	0.10	0.93	elastin; Eln	U08210	elastin precursor (tropoelastin).	major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely.	575.0 cM		Kinase	*
Msa.6386.0	1.00	1.42	-3.46	2.04	-1.35	0.22	-2.64	0.72	-3.21	0.57	mitogen activated protein kinase 13; Mapk13	W13523			17A3-B		Kinase	*
Msa.1160.0	1.00	1.00	17.56	13.65	12.86	11.86	106.21	7.39	107.32	28.80	serum amyloid A 3; Saa3	X03505	serum amyloid a-3 protein precursor.	member of "a" family of apolipoproteins that are differentially expressed. some represent acute phase proteins in the response to inflammatory stimuli. one acts as a precursor of the amyloid a protein, a major constituent of amyloid precipitate.	723.5 cM	Extracellular Protein		*

# Table 2001

X03479	1.00	-1.29	13.98	9.47	18.92	17.89	104.27	16.64	92.13	20.20	Serum amyloid A 3; Saa3	X03479	Serum amyloid a-3 protein precursor.	Serum amyloid a proteins (saa) constitute a family of apolipoproteins that are differentially expressed. some family members represent acute phase proteins in the response to inflammatory stimuli. one of these acts as a	723.5 cM	Extracellular Protein	*
U73004	1.00	4.48	15.01	7.85	9.35	4.84	56.63	17.17	86.24	20.61	secretory leukocyte protease inhibitor; Slpi	U73004	antileukoprotease 1 precursor (alp) (secretory leukocyte protease inhibitor).	acid-stable proteinase inhibitor with strong affinities for trypsin, chymotrypsin, elastase, and cathepsin g; may prevent elastase-mediated damage to oral and possibly other mucosal tissues. associated with wound healing due to its inhibition of		Proteolytic	*
M83219	1.00	8.84	25.35	7.26	17.08	10.37	45.22	2.88	62.94	10.24	S100 calcium-binding protein A9 (calgranulin B); S100a9	M83219	calgranulin b (migration inhibitory factor-related protein 14) (mrp-14) (p14) (leukocyte 11 complex heavy chain).	expressed by macrophages in acutely inflamed tissues and in chronic inflammations. seems to be an inhibitor of protein kinases. also expressed in epithelial cells constitutively or induced during dermatoses. may interact with	343.6 cM	Cytokine	*
U27267	1.00	1.00	9.77	7.32	6.29	5.29	46.55	3.12	52.23	16.41	small inducible cytokine B subfamily, member 5; Scyb5	U27267	small inducible cytokine b5 precursor (cytokine lix).	may participate in the recruitment of inflammatory cells by injured or infected tissue. involved in neutrophil activation	553.0 cM	Cytokine	*

# FOET "T54E200T"

Msa.2129.0	1.00	2.49	9.94	3.74	4.24	3.09	49.39	3.66	45.88	11.97	lipocalin 2; Len2	W13166	neutrophil gelatinase-associated lipocalin precursor (ngal) (p25) (sv-40 induced 24p3 protein).	acute phase forms a covalently linked, disulfide-bridged heterodimer with the 92 kd type v collagenase (mmp-9). neutrophil gelatinase-associated lipocalin 2,25kda, found at moderate levels, only in breast and lung. component of human tear (lipophilic ligand carrier protein suprefamily, lipocalin family, kemal group), modulator of inflammation, involved in the	2 27.0 cM	Extracellular Protein		*
J04596	1.00	1.16	6.78	5.34	3.06	1.86	25.23	2.49	37.61	11.33	GRO1 oncogene; Gro1	J04596	growth regulated protein precursor (platelet-derived growth factor-inducible protein (kc) (secretory protein α51).	has chemotactic activity for neutrophils. contributes to neutrophil activation during inflammation (hvs stimulant).	5 51.0 cM	Extracellular Protein		*
Z27231	1.00	2.87	3.52	2.37	10.54	8.59	22.63	6.04	32.08	4.73	matrix metalloproteinase 9; Mmp9	Z27231	92 kda type iv collagenase precursor (ec 3.4.24.35) (92 kda gelatinase) (matrix metalloproteinase-9) (mmp-9) (gelatinase b) (gelb).	regulator in matrix remodeling, expressed in alveolar macrophages and granulocytes, key regulator of growth plate angiogenesis and apoptosis of hypertrophic chondrocytes in mice, and involved in the	2 96.0 cM	Metabolic		*
M15131	1.00	1.55	5.35	3.53	5.53	4.53	28.75	3.16	31.62	8.61	interleukin 1 beta; Il1b	M15131	interleukin-1 beta precursor (il-1 beta).	produced by macrophages and monocytes, it is required for the interaction between antigen-presenting cells and lymphocytes initiating an immune response. it can also be produced from a number of other cells and is involved in a	2 73.0 cM	Cytokine		*

# Introduction

	1.00	-1.04	3.76	3.44	6.56	7.79	26.89	1.34	30.00	4.34	matrix metalloproteinase 3; Mmp3	X66402	stromelysin-1 precursor (ec 3.4.24.17) (matrix metalloproteinase-3) (mmp-3) (transin-1) (sl-1).	the stromelysins are metalloproteinase enzymes (ec 3.4.24.17) involved in the metabolism of components of the extracellular matrix	9 1.0 cM	Proteolytic
AA638539	1.00	1.84	7.52	3.14	1.82	0.25	14.69	4.30	26.78	8.36	DNA segment, Chr 5, Wayne State University 111, expressed; DSWasu11le	AA638539			5 54.0 cM	EST; Unknown
Msa.27241.0	1.00	1.00	3.58	2.53	4.68	0.44	14.73	7.02	23.04	4.95	insulin-like growth factor binding protein 4; Igfbp4	AA066368	insulin-like growth factor binding protein 4 precursor (igfbp-4) (lbp-4) (shown to either inhibit or stimulate the growth promoting effects of the igfs on cell culture. they alter the interaction of igfs with their cell surface receptor)	igf-binding proteins prolong the half-life of the igfs and have been shown to either inhibit or stimulate the growth promoting effects of the igfs on cell culture. they alter the interaction of igfs with their cell surface receptor		
M58288	1.00	1.00	4.46	2.99	2.92	1.92	23.86	0.91	21.79	6.27	colony stimulating factor 3 receptor (granulocyte); Csf3r	M58288	granulocyte colony stimulating factor receptor precursor (g-csf-r).	receptor for granulocyte colony-stimulating factor (g-csf). in addition it may function in some adhesion or recognition events at the cell surface.	4 57.5 cM	Receptor
M99054	1.00	1.38	2.39	1.33	14.56	12.33	20.35	11.20	21.54	4.48	acid phosphatase 5, tartrate resistant (TRAP); Acp5	M99054	tartrate-resistant acid phosphatase type-5 precursor (ec 3.1.3.2) (tr-ap) (tartrate-resistant acid apase) (taranase)	aka trap (in mouse, not human) -- a lysosomal enzyme and marker of osteoclasts.	9 6.0 cM	Intracellular Protein
M83218	1.00	9.16	8.77	1.81	9.30	6.50	15.39	2.10	20.18	0.81	S100 calcium binding protein A8 (calgranulin A); S100a8	M83218	calgranulin a (migration inhibitory factor-related protein 8) (mmp-8) (p8) (leukocyte II complex light chain) (chemotactic cytokine cp-10) (pro inflammatory s100 cytokine).	expressed by macrophages in chronic inflammations. also expressed in epithelial cells constitutively or induced during dermatoses. may interact with components of the intermediate filaments	3 43.6 cM	Cytokine



# Table 1 "Table 2001"

X94353	1.00	4.36	6.28	1.96	3.34	0.80	3.60	1.19	14.16	0.37	cathelin-like protein; Cnlp	X94353	cathelin-related antimicrobial peptide precursor (cramp) (cathelin-like protein) (clp)	acts as a potent antimicrobial peptide.	9 61.0 cM	Metabolic	
Msa.38664.0	1.00	1.00	3.40	0.91	2.76	1.76	5.71	1.59	13.90	3.18		AA144469				EST; Unknown	
W49204	1.00	1.24	7.53	2.19	6.24	4.95	7.85	4.84	13.67	4.24	glypican 1; Gpc1	W49204					
X66473	1.00	1.79	0.70	1.41	2.92	4.00	10.73	1.24	13.46	1.70	matrix metalloproteinase 13; Mmp13	X66473	collagenase 3 precursor (ec 3.4.24.7) (matrix metalloproteinase-13) (mmp-13).	degrades collagen type I, does not act on gelatin or casein. could have a role in tumoral process. regulator of matrix remodeling component of the mmp cluster, expressed in the synovial membrane and synovial fibroblasts. a novel myeloid-specific granule protein related to porcine cathelin, but showing important structural differences. this may represent the first isolated member of a new cystatin family. more importantly, the small size of the protein binds to p-, e- and l-selectins. the calcium-dependent high affinity interaction with p-selectin mediates the tethering and rolling of neutrophils and lymphocytes on endothelial cells.	9	Proteolytic	
L37297	1.00	2.53	6.23	1.63	2.38	0.66	3.08	1.11	12.74	1.56	neutrophilic granule protein; Ngp	L37297				Intracellular Protein	
X91144	1.00	2.10	3.53	1.24	4.04	2.92	10.33	0.54	12.68	2.95	selectin, platelet (p-selectin) ligand; Selp1	X91144	p-selectin glycoprotein ligand 1 precursor (psgl-1) (selectin p ligand).	binds to p-, e- and l-selectins. the calcium-dependent high affinity interaction with p-selectin mediates the tethering and rolling of neutrophils and lymphocytes on endothelial cells.	5 64.0 cM	Extracellular Protein	
X54542	1.00	1.37	2.99	1.71	1.36	0.24	8.15	2.35	12.39	3.14	interleukin 6; Il6	X54542	interleukin-6 precursor (il-6) (interleukin hp-1) (b cell hybridoma growth factor).	il6 may be the most extremely pleiotropic of cytokines, with a broad range of activities on different cell types.	5 17.0 cM	Cytokine	

# Table 1: The 2007

X81627	1.00	1.92	3.27	1.14	2.57	0.96	12.19	0.13	11.79	2.91	lipocalin 2; Lcn2	X81627	neutrophil gelatinase-associated lipocalin precursor (ngal) (p25) (sv-40 induced 24h3)	capable of carrying small lipophilic molecules like retinol, steroids, and odorants.	2 27.0 cM	Extracellular Protein		*
ET62052	1.00	1.06	5.14	2.14	3.73	0.87	3.52	1.29	11.69	0.43	immunoglobulin heavy chain 4 (serum IgG1); Igh-4	ET62052	myeloperoxidase precursor (ec 1.11.1.7) (mpo).	this enzyme is present in primary granules of neutrophils and plays a major role in the oxygen- dependent microbicidal system of granulocytes.	12 58.0 cM			*
W44075	1.00	1.61	5.43	2.30	3.25	1.18	3.35	1.14	11.54	2.21	myeloperoxidase; Mpo	W44075	myeloperoxidase precursor (ec 1.11.1.7) (mpo).	this enzyme is present in primary granules of neutrophils and plays a major role in the oxygen- dependent microbicidal system of granulocytes.	11 49.0 cM	Intracellular Protein		*
Msa.6242.0	1.00	-1.69	-1.10	2.37	4.33	3.18	8.04	2.31	10.59	1.01	cathepsin K; Ctsk	W13263	cathepsin k precursor (ec 3.4.22.38).	closely involved in osteoclastic bone resorption and may participate partially in the disorder of bone remodeling. displays potent endoprotease activity against fibrinogen at acid ph. may play an important role in extracellular matrix degradation.	3 47.9 cM	Proteolytic		*
U59488	1.00	1.09	2.63	0.99	2.49	0.01	12.29	1.48	9.98	2.50	neutrophil cytosolic factor 4; Ncf4	U59488	neutrophil cytosol factor 4 (ncf-4) (neutrophil nadph oxidase factor 4) (p40-phox) (p40phox).	nadph oxidase consists of proteins p47-phox, p67-phox, p4-phox, and a small regulatory g protein. p4-phox is not required for oxidase activity and has been proposed to have a regulatory function.	15 47.2 cM	Intracellular Protein		*
Z12297	1.00	-1.13	2.36	1.52	2.47	4.30	14.05	0.57	9.42	1.82	small inducible cytokine A7; Scya7	Z12297	small inducible cytokine a7 precursor (monocyte chemoattractant protein 3) (mcp-3) (monocyte chemoattractant protein 3) (intercrine/chemokine).	chemotactic factor that attracts monocytes and eosinophils, but not neutrophils. augments monocyte anti-tumor activity (by similarity). also induces release of gelatinase b. binds to ccr1, ccr2, ccr3.	11 46.5 cM	Cytokine		*



# Table 10

C76739	1.00	1.00	1.85	1.03	2.46	3.48	12.67	2.14	9.30	2.34	macrophage C-type lectin, Mpl	C76739		a type ii transmembrane protein with a single extracellular c-type lectin domain. expressed in cell lines and normal mouse tissues in a macrophage-restricted manner	6 56.5 cM	Cell Surface Protein	
U60438	1.00	1.09	2.36	0.99	2.45	1.31	17.95	6.58	8.54	2.10	serum amyloid A 2; Saa2	U60438	serum amyloid a-2 protein precursor [contains: amyloid protein a (amyloid fibril protein aa)]	saa1, saa2, and saa3 encode acute phase response proteins in response to inflammatory stimuli. acts as a precursor of the amyloid a protein that is a major constituent of amyloid fibrils formed in secondary amyloidosis	7 23.5 cM	Other	
X94444	1.00	-1.35	-0.12	1.31	3.13	2.06	5.71	1.36	8.43	0.90	cathepsin K; Ctsk	X94444	cathepsin k precursor (ec 3.4.22.38).	cathepsin k (ec 3.4.22.38), encoded in the mouse by ctsk, is implicated in bone resorption. expression is predominantly in osteoclasts; embryonic expression also takes place in some hypertrophic chondrocytes of growth cartilage	3 47.9 cM	Proteolytic	
M73748	1.00	-1.54	1.94	0.96	2.06	0.54	9.36	1.95	8.21	1.69	glycoprotein 38; Gp38	M73748	glycoprotein 38 precursor (gp38) (cds-8)			Cell Surface Protein	
X83601	1.00	1.04	0.95	1.04	1.89	3.72	14.68	1.06	8.18	2.71	pentaxin related gene; Ptx3	X83601	pentaxin-related protein ptx3 precursor (tumor necrosis factor-inducible protein tsg14)	a tnfr stimulated gene. produced outside of the liver, increased levels of expression are induced by lps.	3 33.8 cM	Extracellular Protein	
X96639	1.00	-1.20	1.41	0.88	1.95	0.27	4.72	1.16	8.11	2.12	exostosin (multiple 1; Ext1)	X96639	exostosin-1 (putative tumor suppressor protein ext1) (multiple exostosin protein 1)	appears to be a tumor suppressor.	15 26.55 cM	Other	

# Table 1

C80103	1.00	-1.06	1.60	0.88	3.45	2.25	8.46	0.69	7.56	1.13	plastin 2, L; Pls2	C80103	I-plastin (lymphocyte cytosolic protein 1) (lcp-1) (65 kda macrophage protein) (m65)	actin-bundling protein.		Intracellular Protein	
M25324	1.00	1.00	1.80	0.68	1.26	0.26	6.55	1.35	7.55	2.74	selectin, lymphocyte; Sell	M25324	I-selectin precursor (lymph node homing receptor) (leukocyte adhesion molecule-1) (lam-1) (ly-22) (lymphocyte surface mel-14 antigen) (leukocyte-endothelial cell adhesion molecule 1) (lucama1) (cd62L)	cell surface adhesion protein. mediate the adherence of lymphocytes to endothelial cells of high endothelial venules in peripheral lymph nodes.	1 86.6 cM	Cell Surface Protein	
C80638	1.00	-1.07	0.91	0.65	1.97	0.69	7.94	3.14	7.51	1.81	EST; Unknown	C80638				EST; Unknown	
Msa.24575.0	1.00	1.03	0.77	0.72	2.95	0.34	6.02	0.16	7.13	1.48	EST	W82261				EST; Unknown	
Msa.1271.0	1.00	1.60	2.92	0.86	1.26	0.15	1.35	0.13	6.94	0.84	lactotransferrin; Lif	J03298	lactotransferrin precursor (lactoferrin).	transferrins are iron binding transport proteins which can bind two atoms of ferric iron in association with the binding of an anion, usually bicarbonate.	9 61.0 cM	Intracellular Protein	
AA200615	1.00	-1.21	0.51	1.06	2.69	0.23	4.76	1.05	6.94	0.92	homologue of GENESEQN/Z36322 Mechanical stress induced cDNA encoding protein 608	AA200615		patent held by quark biotech, inc. - identification of stress induced genes for determining risk and preventing, treating or controlling osteoporosis		Other	
Msa.136.0	1.00	-1.02	1.05	0.73	2.34	1.16	4.34	0.20	6.84	1.15	interleukin 2 receptor, gamma chain; IL2rg	U21795	cytokine receptor common gamma chain precursor (gamma-c) (interleukin-2 receptor gamma chain) (il-2r gamma chain) (m64)	common subunit for the receptors for a variety of interleukins.	X 38.0 cM		

# FOCUS "E54E2001"

Msa.739.0	1.00	-1.82	-1.01	2.43	0.89	2.70	6.58	0.93	6.75	0.72	haptoglobin; Hp	M96827		haptoglobin combines with free plasma hemoglobin, preventing loss of iron through the kidneys and protecting the kidneys from damage by hemoglobin, while making the hemoglobin accessible to degradation	8 55.0 cM	Extracellular Protein	
D37837	1.00	1.26	1.48	0.88	2.18	0.80	5.85	1.31	6.34	1.47	plastin 2, L; Pls2	D37837	I-plastin (lymphocyte cytosolic protein 1) (lep-1) (65 kDa macrophage protein) (m65)	actin-bundling protein.		Structural Protein	
UI7961	1.00	1.15	4.42	0.90	3.16	1.65	7.12	1.45	6.33	1.79	src associated in mitosis, 68 kDa; Sam68	UI7961					
U83903	1.00	-1.40	0.77	1.17	1.33	3.57	8.40	3.12	6.29	0.55	tumor necrosis factor induced protein 6; Tnfrp6	U83903		induced in vitro in several cell types by proinflammatory cytokines, and in vivo in pathological conditions such as rheumatoid arthritis. interacts with link protein and aggrecan. involved in matrix dissociation and regulated by ph	2	Regulatory	
M59378	1.00	1.72	2.24	0.60	2.28	1.03	7.57	0.87	6.26	1.20	tumor necrosis factor receptor superfamily, member 1b; Tnfrsf1b	M59378	tumor necrosis factor receptor 2 precursor (tnfr-2) (p75).	encodes the larger of two receptors for the tumor necrosis factor. its expression is regulated by external factors. a tnfrsf1b targeted null mutation shows normal t-cell development and activity, but is resistant to tnfr-induced cell death	4 75.5 cM	Receptor	

# Table 2

U16985	1.00	1.02	1.86	0.93	1.83	0.19	5.30	0.24	6.23	1.04	lymphotoxin B; Ltb	U16985	lymphotoxin-beta (tumor necrosis factor c).	member of the tnfr ligand family isolated from human t cells. only found on the cell surface, where it forms a 2:1 trimeric complex with lymphotoxin a. constitutively expressed in lymphoid and hematopoietic tissues, maximal in thymic medulla and splenic white pulp may play a specific role in immune response regulation. provides the membrane anchor for the attachment of the	17 19.06 cM	Cytokine	
Msa.1700.0	1.00	2.40	-0.32	0.82	2.12	3.77	5.59	2.04	5.93	0.88	phospholipase A2 group VII (platelet-activating factor acetylhydrolase, plasma); Pla2g7	U34277	platelet-activating factor acetylhydrolase precursor (ec 3.1.1.47) (paf acetylhydrolase) (paf 2-acetylhydrolase) (ldl-associated phospholipase a2) (ldl-pla(2)) (2-acetyl-1-alkylglycerophosphocholine esterase) (1-alkyl-2-acetyl-glycerophosph	modulates the action of platelet-activating factor (paf) by hydrolyzing the sn-2 ester bond to yield the biologically inactive lyso-paf. has a specificity for substrates with a short residue at the sn-2 position. it is inactive against lo		Cytokine	
AA059883	1.00	-1.03	0.28	1.16	3.05	4.37	8.59	2.30	5.91	0.99	angiopoietin related	AA059883		the region of this genomic sequence that contains this sequence is listed as angiopoietin related.		Hemostasis	

# Protein Data Bank

U05837	1.00	-1.30	0.82	0.94	3.68	2.47	5.23	1.66	5.79	1.04	hexosaminidase A; Hexa	U05837	beta-hexosaminidase alpha chain precursor (ec 3.2.1.52) (n-acetyl-beta-glucosaminidase) (beta-n-acetylhexosaminidase) (hexosaminidase a).	lysosomal enzymes that contribute to the degradation of glycoproteins, glycolipids, and glycosaminoglycans. widely expressed, associated with ganglioside degradation. absence of the b form is associated with the gene are found at a high level in mature human and murine macrophages and at a moderate level in certain myelomonocytic cell lines	9 29.0 cM	Proteolytic	
Msa.1600.0	1.00	1.12	-0.54	1.14	0.56	2.11	4.88	0.13	5.61	0.65	macrophage expressed gene 1; Mpeg1	L20315		transcripts from the gene are found at a high level in mature human and murine macrophages and at a moderate level in certain myelomonocytic cell lines		EST; Unknown	
L32974	1.00	-2.05	1.79	0.94	0.01	1.10	1.71	0.31	5.57	1.47	interferon-induced protein with tetrapeptide repeats 3; Ifit3	L32974	interferon-induced protein with tetrapeptide repeats 3 (ifit-3) (glucocorticoid-attenuated response gene 49 protein) (carr-49) (lrr2)				
AA387033	1.00	1.17	1.46	0.66	2.73	1.63	5.21	0.80	5.54	0.46	Unknown	AA387033				EST; Unknown	
U72643	1.00	1.61	0.59	0.80	0.84	2.13	5.65	0.13	5.50	0.94	leucocyte specific transcript 1; Lst1	U72643		defense/immunity protein, an integral membrane protein.	17 19.06 cM	EST; Unknown	
AA174982	1.00	-1.02	1.24	0.85	3.75	2.69	5.03	1.76	5.39	0.63	coronin, actin binding protein 1A; Coro1a	AA174982	coronin-like protein p57 (coronin 1a) (fragment).	the remodelling of the cortical actin cytoskeleton that is responsible for phagocytosis and macropinocytosis. in mammalian neutrophils, a coronin-like protein is also associated with the cytoskeleton	7 62.5 cM	Intracellular Protein	

# Table 20

U54984	1.00	-1.57	0.54	1.35	2.53	1.39	3.75	0.53	5.33	0.29	matrix metalloproteinase 14 (membrane-inserted); Mmp14	U54984	matrix metalloproteinase-14 precursor (ec 3.4.24.-) (mmp-14) (membrane-type matrix metalloproteinase 1) (mt-mmp 1) (mmp1).	expressed in invasive lung carcinoma cells, induces activation of gelatinase a on the cell surface and enhances cell invasion of basement membrane. specifically activates pro-gelatinase a. may trigger invasion by tumor cells by	14 12.5 cM	Proteolytic	
L38281	1.00	-0.02	1.46	0.32	1.28	0.28	3.32	0.69	5.28	1.51	immunoresponsive gene 1; Irg1	L38281	immune-responsive protein 1		14 53.5 cM		
AA245242	1.00	-1.73	1.18	0.56	2.72	1.42	4.17	0.72	5.23	0.51	MARCKS-like protein; Mlp	AA245242	cardiac (muscle lim protein) (cysteine-rich protein 3) (crp3), marcks-related protein (marcks) (brain protein f52)	binds calmodulin and is a substrate for protein kinase c	4 59.0 cM	Signal Transduction	
AA183642	1.00	1.24	1.21	0.76	0.87	2.08	9.10	1.34	5.10	0.86	Unknown; EST	AA183642				EST;	
AA472322	1.00	1.00	3.10	0.52	2.32	1.32	6.68	0.28	5.09	1.40	EST; Unknown	AA472322				EST;	
X16133	1.00	-1.08	-0.57	1.49	-1.41	0.16	5.06	0.35	4.88	0.56	proteoglycan, secretory granule; Prig	X16133	secretory granule proteoglycan core protein precursor (mastocytoma proteoglycan core protein) (serglycin)	core protein for highly acidic proteoglycan containing glycosaminoglycan that are almost exclusively		Intracellular Protein	
Msa.15534.0	1.00	-1.34	1.53	0.34	1.95	0.05	2.92	0.95	4.85	0.93	neutrophil cytosolic factor 2; Ncf2	W71124		chondroitin sulfate c	1 76.1 cM		
Msa.22604.0	1.00	-1.06	-0.19	0.75	1.49	0.45	2.41	0.16	4.81	0.70		AA036297					
X61800	1.00	4.66	1.50	0.81	1.67	4.17	4.45	1.29	4.80	0.48	CCAAT/enhancer binding protein (C/EBP), delta; Cebpδ	X61800	ccat/enhancer binding protein delta (c/ebp delta) (c/ebp-related protein 3).	a transcription factor that binds to cis-regulatory dna sequences of viral genes and regulatory sequences of cellular genes that encode ma. important transcriptional activator in the regulation of genes involved in immune	16 9.0 cM	Transcription Factor	

# Table 200

AA408170	1.00	2.81	3.78	0.59	3.24	1.50	5.10	0.95	4.80	1.06	DEAD (aspartate-glutamate-alanine-aspartate) box polypeptide, Y chromosome: Dhy 13, Abbot 1 expressed (TM7SF1)	AA408170			Y 2.07 cM	EST; Unknown	
C80550	1.00	-2.09	0.70	0.65	1.34	0.18	4.20	0.44	4.78	1.27	RAS-related C3 botulinum substrate 2; Rac2	C80550		seven transmembrane domain protein, upregulated during kidney development.		Cell Surface Protein	
X53247	1.00	-1.36	0.91	0.62	0.75	1.80	3.63	0.14	4.77	0.85	RAS-related C3 botulinum substrate 2; Rac2	X53247		murine homolog of a class of human ras-related proteins that are substrates for adenylylation by botulinum toxin c3 adp-ribosyltransferase. expression is restricted to hematopoietic cells and organs. seems to be involved in the		Signal Transduction	
M32370	1.00	-1.06	0.19	1.08	0.85	2.16	6.33	1.87	4.76	0.60	SFV proviral integration 1; Spil	M32370		31 kda transforming protein (transcription factor pu.1).	2 47.5 cM	Transcription Factor	
Msm.23838.0	1.00	-1.57	-1.50	1.20	0.38	3.42	3.77	0.52	4.66	1.00	tumor necrosis factor induced protein 6; Tnfrp6	AA051341		induced in vitro in several cell types by proinflammatory cytokines, and in vivo in pathological conditions such as rheumatoid arthritis. interacts with link protein and aggrecan. involved in matrix dissociation and regulated by ph	2	Regulatory	

Msa.2530.0	1.00	1.00	1.30	0.30	1.23	0.23	5.83	1.26	4.66	1.14	vav oncogene; Vav	X64361	vav proto-oncogene; cell surface glycoprotein mac-1 alpha subunit precursor (cr-3 alpha chain) (cd11b) (leukocyte adhesion receptor mol) (integrin alpha m).	probable exchange factor for a small ras-like gtp-binding protein. can be activated by truncation of the n-terminus.	17 32.7 cM	Signal Transduction	*
X07640	1.00	-1.80	1.45	0.57	0.02	1.79	4.71	1.02	4.65	0.90	integrin alpha M (Cd11b); Igam	X07640	cell surface glycoprotein mac-1 alpha subunit precursor (cr-3 alpha chain) (cd11b) (leukocyte adhesion receptor mol) (integrin alpha m).	mac-1 is a cell surface glycoprotein of monocytes, macrophages and granulocytes which has been implicated in various adhesive interactions of these cells as well as in mediating the uptake of complement-coated particles. mac-1 is identical with cr-3, the receptor for the ic3b fragment of the third complement component. mac-1 probably recognize the		Cell Surface Protein	*
Msa.641.0	1.00	-1.03	-0.19	1.41	1.05	2.42	4.35	0.06	4.63	0.84	Fc receptor, IgE, high affinity I, gamma polypeptide; Fcεr1g	W41745	high affinity immunoglobulin epsilon receptor gamma-subunit precursor (fcεr1) (ige fc receptor, gamma-subunit) (fc-εr1) (FcγRIIIa)	the gamma subunit has a critical role in allowing the ige fc receptor to reach the cell surface	193.3 cM	Receptor	*
D10911	1.00	-1.22	1.65	0.35	2.18	1.00	4.95	0.08	4.59	0.99	a disintegrin and metalloprotease domain (ADAM) 8; Adam8	D10911	adam 8 precursor (ec 3.4.24.-) (a disintegrin and metalloproteinase domain 8) (cell surface antigen ms2) (macrophage cysteine-rich glycoprotein) (cd156 antigen)	possible involvement in extravasation of leukocytes.	7 F3-F5	Proteolytic	*
X15591	1.00	1.53	0.39	0.89	0.63	1.86	3.57	0.27	4.58	0.64	cytotoxic T lymphocyte-associated protein 2 alpha; Ctlα2a	X15591	ctla-2-alpha protein precursor.	not known, expressed in activated t-cell.	13 36.0 cM	Cell Surface Protein	*



# TABLE 1

AA285691	1.00	1.21	0.98	0.77	2.15	3.40	6.67	2.62	4.57	0.72	cytohesin binding protein (Cbp)	AA285691			bone marrow-derived dendritic cells"" cloned by subtraction of activated bone marrow macrophage versus bone marrow-derived dendritic cells""		Cell Surface Protein	
Msa.1529.0	1.00	1.00	0.58	0.47	0.44	0.64	2.46	0.31	4.50	0.60	growth factor receptor bound protein 10; Grb10	U18996	growth factor receptor-bound protein 10 (grb10 adaptor protein).	11.8.0 cM	plays a functional role in insulin and igf-i signaling. may serve to positively link the insulin and igf-i receptors to an uncharacterized mitogenic signaling pathway. interacts with the cytoplasmic domain of the autophosphorylated insulin receptor which is then inhibited. the interaction is mediated by the sh2 domain. also binds activated platelet-derived growth factor receptor and epidermal growth	Signal Transduction		
X67783	1.00	2.51	0.70	0.76	0.80	1.94	2.37	0.17	4.49	0.49	vascular cell adhesion molecule 1; Vcam1	X67783	vascular cell adhesion protein 1 precursor (v-cam 1).	3.50.8 cM	cell-cell recognition. appears to function in leukocyte-endothelial cell adhesion. interacts with beta-1 integrin via4 on leukocytes, and mediates both adhesion and signal transduction. vcam1/via4 interaction may play a pathophysiologic role	Cell Surface Protein		
X81582	1.00	-1.60	-0.48	1.27	0.82	2.27	2.74	0.12	4.48	0.38	insulin-like growth factor binding protein 4; Igfbp4	X81582	insulin-like growth factor binding protein 4 precursor (igfbp-4)					

# Table "Leukocyte"

Msa.2034.0	1.00	-1.02	0.25	0.81	1.38	2.45	5.16	0.29	4.46	0.72	CD53 antigen; Cd53	X97227	leukocyte surface antigen cd53 (cell surface glycoprotein cd53).	may be involved in growth regulation in hematopoietic cells.	3 50.5 cM	Cell Surface Protein		*
AA103744	1.00	-1.31	1.73	1.20	3.98	2.12	7.13	2.86	4.42	0.81	ribosomal protein L27a; Rpl27a	AA103744	60S ribosomal protein L27a (L29).	plays cardinal role in calcium metabolism, and may be involved in neural transmission. buffers cytosolic calcium. may stimulate a membrane ca(2+)-atpase and a 3',5'-cyclic nucleotide phosphodiesterase. expressed in many tissues.	7 E2-F1	Metabolic		*
AA189487	1.00	1.16	0.09	0.68	1.28	2.89	4.40	1.72	4.39	0.91	sushi-repeat-containing protein; X chromosome; SrpX-peptide	AA189487				EST; Unknown		*
Msa.1843.0	1.00	-1.25	0.33	0.73	0.53	1.90	5.85	0.19	4.32	1.17	chemokine (C-C) receptor 1; chemokine (C-C) receptor 1-like 2; Cmkbr1, Cmkbr112	U28404	c-c chemokine receptor type 1 (c-c ckr-1) (cc-ckr-1) (ccr-1) (ccr1) (macrophage inflammatory protein-1 alpha receptor) (mip-1alpha-r) (rantes-r); probable c-c chemokine receptor type 3 (c-c ckr-3) (cc-ckr-3) (ccr-3) (ccr3) (ckr3) (macrophage inflammatory protein-1 alpha receptor-like 2)	mip-1a-receptor. all three of the cmkbr1 genes has been found in leukocytes, but their patterns of expression differ in solid organs. cmkbr1 is expressed in heart, spleen, and lung;	9 72.0 cM	Receptor		*
Msa.31660.0	1.00	-1.04	0.86	0.72	0.81	2.03	4.38	0.48	4.28	0.73	CD53 antigen; Cd53	AA105582	leukocyte surface antigen cd53 (cell surface glycoprotein cd53).	may be involved in growth regulation in hematopoietic cells.	3 50.5 cM	Cell Surface Protein		*
U29947	1.00	-1.41	-2.19	1.91	3.44	5.25	7.01	4.87	4.27	1.44	mannosidase 2, alpha B1; Man2b1	U29947	lysosomal alpha-mannosidase precursor (ec 3.2.1.24) (mannosidase, alpha b) (lysosomal acid alpha-mannosidase) (laman)	necessary for the catabolism of n-linked carbohydrates released during glycoprotein turnover. cleaves all known types of alpha-mannosidic linkages.	8 37.0 cM	Regulatory		

\*

AA546670	1.00	-2.14	0.74	0.79	2.40	1.24	3.20	0.63	4.20	0.32	myristoylated alanine rich protein kinase C substrate; Macs	AA546670	myristoylated alanine-rich c-kinase substrate (marcks).	marcks is the most prominent cellular substrate for protein kinase c. this protein binds calmodulin, actin, and synapsin. marcks is a filamentous (f) actin cross-linking protein.	10 22.0 cM		
Msa.40979.0	1.00	-1.35	2.97	0.90	1.29	2.51	3.55	1.17	4.19	1.07		AA161769					
AA544540	1.00	-1.10	2.67	0.86	2.10	1.04	4.47	1.05	4.18	0.85		AA544540					
Msa.1099.0	1.00	1.13	0.92	0.61	2.24	0.74	3.25	0.27	4.15	0.40	neuron specific gene family member 1; Nsg1	W46015	neuron specific protein family member 1 (brain neuron cytoplasmic protein 1) (p21) (m234).		5 21.0 cM	EST; Unknown	
U36993	1.00	1.03	0.47	0.64	0.33	1.42	4.96	1.07	4.12	0.97	cytochrome P450, 7b1; Cyp7b1	U36993	cytochrome p450 7b1 (oxysterol 7-alpha-hydroxylase) (ec 1.14.13.-) (hct-1).	heme-containing enzymes involved in metabolism of a number of endogenous substrates. expressed principally in brain, only low levels found in liver. most closely resembles p450vital, cholesterol 7 a hydroxylase, but almost different from it.	3 1.0 cM	Metabolic	
AA170444	1.00	1.16	1.10	0.52	1.15	0.07	2.61	0.32	4.04	0.68	EST; Unknown	AA170444				EST; Unknown	
AA289661	1.00	-1.32	0.82	0.90	1.52	2.69	4.34	0.86	4.01	0.60	EST; Unknown	AA289661				EST; Unknown	
K01496	1.00	-1.66	0.56	0.76	1.77	3.25	4.14	1.13	4.01	0.40	histocompatibility 2, complement component factor B; H2-Bf	K01496	complement factor b precursor (ec 3.4.21.47) (c3/c5 convertase).	factor b which is part of the alternate pathway of the complement system is cleaved by factor d into 2 fragments: ba and bb. bb, a serine protease, then combines with complement factor 3b to generate the c3 or c5 convertase.	17 18.85 cM	Hemostasis	

# Table 1: Gene Ontology

AA189758	1.00	-1.21	1.44	0.52	2.27	1.23	5.25	0.42	4.00	0.32	Wbcr5 gene product; Wbcr5	AA189758	(see note) contains two lim domains and a putative protein kinase domain. high expression levels in ens, particularly in spinal cord, cranial nerve and dorsal root ganglia. lesser expression in heart and skeletal muscle. may be associated with			
U88328	1.00	1.73	0.18	0.87	1.95	4.32	5.37	1.50	4.00	0.28	cytokine inducible SH2-containing protein 3 (SOCS3); Cish3	U88328	cytokine inducible sh2-containing protein 3 (protein effector 10).	ECM (Matrix Prot)		
AA015322	1.00	1.70	-1.39	0.77	-0.73	2.09	2.86	2.87	3.98	1.02	SPARC-related protein (SRG) (related to osteonectin)	AA015322		Other		
M13963	1.00	-1.39	2.19	0.75	1.70	0.25	3.64	1.35	3.92	0.80	guanine nucleotide binding protein, alpha inhibiting 2; Gnai2	M13963	the g(i) proteins are involved in hormonal regulation of adenylyl cyclase; they inhibit the cyclase in response to beta- adrenergic stimuli.	Signal Transduction	959.0 cM	
Z16078	1.00	1.06	0.06	1.04	0.83	2.18	3.64	0.16	3.92	0.55	CD53 antigen; Cd53	Z16078	leukocyte surface antigen cd53 (cell surface glycoprotein cd53).	Cell Surface Protein	350.5 cM	
M63836	1.00	-1.50	-0.08	0.81	0.65	2.02	3.88	0.75	3.87	0.12	beta-glucuronidase structural; Gus-s	M63836	aka gusb	Metabolic	572.0 cM	
D11468	1.00	1.82	1.20	0.78	2.26	0.93	0.95	1.00	3.84	1.15	immunoglobulin alpha heavy chain DNA segment, Chr X, Immunex 39, expressed;	D11468		Extracellular Protein		
AA266385	1.00	-1.03	1.00	0.58	1.12	0.04	3.88	0.46	3.84	0.84		AA266385		EST; Unknown		X1.6 cM

# Protein Data Bank

U29762	1.00	3.11	2.20	1.45	5.23	2.30	3.07	1.90	3.83	1.07	D site albumin promoter binding protein; Dbp	U29762	d-site-binding protein (albumin d box-binding protein).	this transcriptional activator recognizes and binds to the sequence 5'-rtatgaag-3' found in the promoter of genes such as albumin, cyp2a4 and cyp2a5. it is not essential for circadian rhythm generation, but modulates important clock output genes. may be a direct target for regulation by the circadian pacemaker component clock. may affect circadian period	7 23.0 cM	Transcription Factor
AA177433	1.00	1.34	0.21	0.82	0.49	2.05	4.56	0.86	3.82	0.51	EST; Unknown	AA177433				EST; Unknown
D28599	1.00	-1.28	0.91	0.59	1.18	0.13	4.59	0.54	3.81	0.96	chondroitin sulfate proteoglycan 2; Cspg2	D28599	versican core protein precursor (large fibroblast proteoglycan)	extracellular matrix link protein.	13 55.0 cM	ECM (Matrix Prot)
D50494	1.00	-2.14	11.79	6.74	3.21	2.21	4.11	1.50	3.78	0.92	DEAD (aspartate-glutamate-alanine-aspartate) box polypeptide 6; Ddx6	D50494	probable apoptosis dependent RNA helicase p54 (oncogene ret homolog) (dead-box protein 6)		9 26.0 cM	
L15443	1.00	1.18	0.10	1.49	2.42	0.90	3.03	0.39	3.78	0.42	membrane component, surface marker 1; M3sl	L15443				Cell Surface Protein
ET62103	1.00	-1.46	10.80	4.19	6.12	8.71	6.88	5.42	3.78	2.72	apoptosis inhibitor 1; birc2 (Apl)	ET62103	inhibitor of apoptosis protein 1 (miap1) (miap-1).	traf1 and/or traf2 associated protein of the iap (inhibitor of apoptosis) family. iaps may play a role in tumour progression rather than tumour initiation, making the iaps an attractive therapeutic target.	9 A2	Regulatory
U88908	1.00	1.55	1.04	0.58	1.90	0.66	5.13	1.33	3.77	0.55		U88908				

\*

AA020512	1.00	1.01	1.31	0.45	1.33	0.02	3.97	0.39	3.75	0.87	caspase 6; Casp6	AA020512	caspase-6 precursor (ec 3.4.22.-) (apoptotic protease mch-2).	involved in the activation cascade of caspases responsible for apoptosis execution. cleaves poly(adp-ribose) polymerase in vitro, as well as lamins. overexpression promotes programmed cell death (by stimulation).	EST; Unknown			
AA172851	1.00	-1.04	0.26	0.77	0.44	1.66	4.53	0.34	3.75	0.58	EST; Unknown	AA172851	atp-binding cassette, sub-family a, member 1 (atp-binding cassette transporter 1) (atp-binding cassette 1) (abc-1)	camp-dependent and sulfonyleurea-sensitive anion transporter. key gatekeeper influencing intracellular cholesterol transport (by similarity)	EST; Unknown	4 23.1 cM		
X75926	1.00	2.26	0.55	0.56	1.93	0.81	2.51	0.07	3.74	0.54	ATP-binding cassette, sub-family A (ABC1), member 1; Abca1	X75926	atp-binding cassette, sub-family a, member 1 (atp-binding cassette transporter 1) (atp-binding cassette 1) (abc-1)	camp-dependent and sulfonyleurea-sensitive anion transporter. key gatekeeper influencing intracellular cholesterol transport (by similarity)	EST; Unknown	4 23.1 cM		
Msa.22134.0	1.00	-1.17	-0.52	1.02	2.09	0.87	3.68	0.40	3.72	0.48	Unknown	AA031158	caspase-11 precursor (ec 3.4.22.-) (ich-3 protease).	involved in the activation cascade of caspases responsible for apoptosis execution. promotes interleukin 1 beta processing by ICE, so may also have a role in inflammatory responses	EST; Unknown			
U59463	1.00	1.12	1.47	0.50	1.56	0.11	3.86	0.75	3.72	0.86	caspase 11; Casp11	U59463	caspase-11 precursor (ec 3.4.22.-) (ich-3 protease).	involved in the activation cascade of caspases responsible for apoptosis execution. promotes interleukin 1 beta processing by ICE, so may also have a role in inflammatory responses	EST; Unknown			
Msa.510.0	1.00	-2.49	-0.90	1.04	0.25	1.81	2.97	0.16	3.71	0.50	histocompatibility 2, complement component factor B; H2-Bf	M57890	complement factor b precursor (ec 3.4.21.47) (c3/c5 convertase).	involved in the alternative or properdin complement pathway	Hemostasis	17 18.85 cM		
AA172673	1.00	1.32	1.17	0.44	1.53	0.29	3.48	0.41	3.70	0.63	paternally expressed gene 3; Peg3	AA172673			EST; Unknown	7 6.5 cM		
AA051505	1.00	-2.70	-1.31	0.66	0.87	2.64	3.03	0.83	3.70	0.72	EST; unknown	AA051505			EST; Unknown			
U89269	1.00	-1.43	0.80	0.75	2.05	3.22	4.88	1.64	3.69	0.60	cathepsin C; Ctsc	U89269	dipeptidyl-peptidase i precursor (ec 3.4.14.1) (dpp-i) (dppi) (cathepsin c) (cathepsin j) (dipeptidyl transferase).	mammalian lysosomal cysteine proteinases. plays a role in protein catabolism within the cell, and may be involved in tumor metastasis. expression is widely distributed, with some variability in level, in mouse tissues.	Proteolytic	7 D3-E1.1		

# Table 2

J03535	1.00	-1.00	0.79	0.72	2.43	1.30	3.93	1.01	3.68	0.20	embigin; Emb	J03535	pou domain, class 6, transcription factor I (octamer-binding transcription factor emb) (transcription regulatory protein mcp-1), teratocarcinoma glycoprotein gp-70 precursor.	embigin and basigin are highly glycosylated transmembrane glycoproteins with two immunoglobulin domains and form a subgroup in the immunoglobulin superfamily. embigin is strongly expressed in the endoderm.	15 57.0 cM	Transcription Factor
AA592768	1.00	1.54	2.46	0.83	4.64	1.76	5.53	2.15	3.66	0.49	small proline-rich protein 2A; Spt2a	AA592768		small proline-rich (spr) proteins are structural components of the cornified cell envelope of stratified squamous epithelia, they are subdivided into three families, i.e., spr1, spr2, and spr3, of which the spr2 family is the most	3 45.2 cM	Structural Protein
AA259937	1.00	-5.79	-1.14	0.85	0.60	2.69	2.67	0.61	3.65	0.51	procollagen, type III, alpha 1; Col3a1	AA259937	collagen alpha (iii) chain precursor.	collagen type iii occurs in most soft connective tissues	1 21.1 cM	ECM (Matrix Prot)
M31419	1.00	1.09	1.63	0.64	1.42	0.20	4.04	0.65	3.65	1.09	interferon activated gene 204; Ifi204	M31419	interferon-activatable protein 204 (ifl-204) (interferon-inducible protein)	member of a cluster of genes activated by interferon on chr 1. function unknown.	1 95.2 cM	Unknown
X13333	1.00	-1.22	-0.21	0.70	0.54	1.83	3.09	0.31	3.65	0.66	CD14 antigen; Cd14	X13333	monocyte differentiation antigen cd14 precursor (lps receptor) (lps-r) (myeloid cell-specific leucine-rich glycoprotein).	a cell surface marker of human monocytes and macrophages. serves as an lps receptor controlling cell activation under physiological conditions. when lps binds to cd14 the cells become activated and release cytokines and	18 31.0 cM	Cell Surface Protein
Msa.17760.0	1.00	1.18	-0.09	0.59	1.30	0.26	2.25	0.17	3.65	0.46		W98059				
Msa.10687.0	1.00	-7.85	-1.32	1.27	0.53	1.55	2.43	0.50	3.62	0.29	Unknown	W48936				EST; Unknown

\* \* \*

# Table 3

D16262	1.00	-2.89	-2.10	0.78	-0.63	1.88	1.84	0.27	3.59	0.99	mesoderm specific transcript; Mest	D16262		aka peg-1 -- the mouse peg1/mest gene is an imprinted gene that is expressed particularly in mesodermal tissues in early embryonic stages	67.5 cM	Cytokine	
M31131	1.00	-1.13	0.01	0.80	0.44	1.57	2.15	0.39	3.58	0.51	cadherin 2; Cdh2	M31131	neural-cadherin precursor (n-cadherin).	cadherins are calcium dependent cell adhesion proteins. they preferentially interact with themselves in a homophilic manner in connecting cells; cadherins may thus contribute to the sorting of heterogeneous cell types. n-cadherin may be involved in	18 6.0 cM	Cell Surface Protein	
AA161790	1.00	-1.89	2.16	0.67	2.68	0.16	3.54	0.34	3.56	0.25	aplysia ras-related homolog A2; Arha2	AA161790		regulates a signal transduction pathway linking plasma membrane receptors to the assembly of focal adhesions and actin stress fibers	237.0 cM	Intracellular Protein	
D83266	1.00	-1.47	0.12	0.69	0.47	1.66	4.05	0.84	3.55	0.78	vav oncogene; Vav	D83266	vav proto-oncogene.	binds to grb2 and grb3	17 32.7 cM	Signal Transduction	*
M35833	1.00	-1.98	-1.06	0.88	0.24	1.52	0.75	0.95	3.54	0.48	midline; Mdk	M35833	midline precursor (retinoic acid-induced differentiation factor).	midline (mkl) is a heparin-binding growth/differentiation factor implicated in the control of development and repair of various tissues. mkl plays important roles in chondrogenesis and contributes to bone	251.0 cM	Cytokine	*



# Topical Proteins

L23801	1.00	-1.89	-2.21	1.27	0.70	2.36	2.59	0.70	3.54	0.51	integrin binding sialoprotein; Ibsp	L23801	bone sialoprotein ii precursor (bsp ii) (cell-binding sialoprotein) (integrin-binding sialoprotein).	aka integrin binding sialoprotein - bone sialoprotein (bsp) is a small, highly posttranslationally modified integrin binding protein found in the mineral compartment of developing bone. contains a conserved arg-gly-asp (rgd) sequence.	556.0 cM	ECM (Matrix Prot)	
U78818	1.00	-2.25	1.14	0.45	1.09	0.02	3.63	0.37	3.54	0.45	downstream of tyrosine kinase 1; Dok1	U78818			634.73 cM		
U19482	1.00	-1.31	1.07	0.85	1.65	2.68	6.02	0.87	3.52	0.32	small inducible cytokine A9; Scya9	U19482	small inducible cytokine a9 precursor (macrophage inflammatory protein 1-gamma) (mip-1-gamma) (macrophage inflammatory protein-related protein-2) (mip-2) (ccf18).	a.k.a mip-1 gamma or ccf18 -- chemokines play an important role in immune and inflammatory responses by inducing migration and adhesion of leukocytes. ccf18 mima is constitutively expressed in macrophage and	1147.4 cM	Cytokine	
U21795	1.00	-1.16	1.05	0.42	1.53	0.36	4.01	0.56	3.51	0.61	interleukin 2 receptor, gamma chain; Il2rg	U21795	cytokine receptor common gamma chain precursor (gamma-c) (interleukin-2 receptor gamma chain) (il-2r; gamma chain) (cd64)	common subunit for the receptors for a variety of interleukins.	X38.0 cM		
M27960	1.00	-1.14	-0.88	1.09	1.29	2.91	5.45	0.51	3.49	0.49	interleukin 4 receptor, alpha; Il4ra	M27960	interleukin-4 receptor alpha chain precursor (il-4r-alpha).	a receptor for il4, a mediator of the th2 (b cell) response. acts as an antagonist to il4, presumably by adsorbing il4 molecules.	762.0 cM	Receptor	
W11156	1.00	0.01	0.61	1.10	1.64	0.10	3.19	0.05	3.49	0.67	EST; unknown	W11156		some similarity to 399 human gamma-interferon-inducible protein		EST; Unknown	

D67076	1.00	-1.17	0.46	0.89	0.18	1.63	3.51	0.21	3.48	0.83	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1; Adamts1	D67076	adam-ts1 precursor (ec 3.4.24.-) (a disintegrin and metalloproteinase with thrombospondin motifs 1) (adamts-1) (adam-ts1).	expression is markedly and selectively induced by lipopolysaccharide administration in the kidney and heart. developmentally regulated membrane proteins containing disintegrin and metalloprotease motifs.	16 53.4 cM	Proteolytic
AA185911	1.00	-1.23	0.41	0.65	1.10	2.48	3.56	0.86	3.47	0.60	lymphocyte antigen 68; Ly68	AA185911				Cell Surface Protein
X84797	1.00	-1.58	0.52	0.66	0.27	1.63	3.78	0.17	3.46	0.43	hematopoietic cell specific Lyn substrate 1; Hcls1	X84797	hematopoietic lineage cell specific protein (hematopoietic cell-specific lyn substrate 1) (lckbp1).	substrate of the antigen receptor-coupled tyrosine kinase. plays a role in antigen receptor signaling for both clonal expansion and deletion in lymphoid cells. directly associates with hax-1, through binding to its c-terminal region. may also be involved in the regulation of gene expression (by	16 B	Hemostasis
ET63188	1.00	-2.00	-1.95	0.95	0.01	1.68	1.62	0.27	3.46	0.42	fibroblast activation protein; Fap	ET63188			2 36.0 cM	Cytokine
Msa.3665.0	1.00	-1.63	-0.56	1.08	0.12	1.68	2.81	0.31	3.45	0.40	DNA segment, Chr 2, Wayne State University 143, expressed; D2Wsu143e	AA116604		cathepsin z, cysteine proteinase, papain superfamily member, ubiquitously expressed, involved normal intracellular degradation.	2 24.0 cM	Proteolytic
U73478	1.00	-1.21	2.43	0.37	2.32	0.99	3.67	0.65	3.42	0.73	acidic nuclear phosphoprotein 32; Ann32	U73478			9 36.0 cM	
Msa.2385.0	1.00	-1.21	-1.71	1.27	0.58	2.13	2.56	0.37	3.41	0.25	insulin-like growth factor binding protein 4; Igfbp4	X81582	insulin-like growth factor binding protein 4 precursor (igfbp-4) (tbp-4) (igf binding protein 4).	binding proteins may act to distribute the igfs among the body fluid compartments, to protect the body from possible hypoglycemic effects of the igfs.		Extracellular Protein
AF003691	1.00	3.40	-1.88	1.54	5.02	3.92	-1.08	1.43	3.41	6.12	keratin-associated protein 14; Krtap14	AF003691				
AA030688	1.00	-1.40	-0.06	0.82	0.38	1.48	5.02	2.01	3.41	0.38	EST; Unknown	AA030688				EST; Unknown

# Table 1

AA189512	1.00	-1.76	0.59	0.90	0.09	1.32	2.95	0.73	3.40	0.81	lymphocyte antigen 86; Ly86	AA189512					
L07063	1.00	-2.99	-1.77	1.08	-0.05	1.46	2.71	0.25	3.39	0.45	FK506 binding protein 6 (65 kDa); Fkbp6	L07063	65 kDa FK506-binding protein precursor (ec 5.2.1.8) (Fkbp65) (Fkbp6) (peptidylprolyl cis-trans isomerase) (ppiase) (rotamase) (immunophilin (Fkbp65)).	aka Fkbp65 -- Fkbp65 is a member of the FK506-binding protein class of immunophilins and is the only member reported to contain four peptidylprolyl cis-trans isomerase domains and an unrelated coob.	11 58.0 cM	Intracellular Protein	
C79010	1.00	-1.16	0.57	0.74	0.20	1.36	2.95	0.16	3.38	0.63	Src-associated adaptor protein; Saps	C79010					??
M16355	1.00	-8.28	0.30	1.12	0.93	2.07	2.65	0.61	3.38	1.03	major urinary protein 1; Mup1	M16355	major urinary protein 1 precursor (mup 1).	the mup proteins are lipocalins, and apparently take part in the transport of pheromones. though secreted in the urine, they are produced in the liver or in the lachrymal, mammary, and submaxillary glands.	4 27.8 cM	Extracellular Protein	
C76049	1.00	1.55	1.84	0.21	1.84	0.32	5.59	0.86	3.38	0.87	EST; Unknown	C76049					EST; Unknown
X80478	1.00	-1.17	-1.47	0.70	0.44	2.11	2.02	0.35	3.38	0.40	AE-binding protein 1; Aebp1	X80478		encodes a 845-aa protein that is almost identical to mouse adipocyte transcription factor acbp1. it is also expressed in a murine osteoblastic line, but is shut off in the final calcification phase, suggesting a transcriptional repressive eff		Transcription Factor	
M87276	1.00	1.13	2.06	0.24	2.43	0.87	2.49	0.07	3.34	0.37	thrombospondin 1; Thbs1	M87276	thrombospondin 1 precursor.	thrombospondin-1 functions as a cell adhesion molecule and also modulates cell movement, cell proliferation, neurite outgrowth and angiogenesis	2 65.0 cM	Extracellular Protein	

D87967	1.00	1.02	0.59	0.61	0.48	1.55	3.41	0.31	3.34	0.33	protein tyrosine phosphatase, non-receptor type substrate 1; Ptpnsl	D87967				273.1 cM	Intracellular Protein	
AA617405	1.00	-1.26	1.56	0.56	1.50	0.41	4.69	0.77	3.32	0.66	EST; Unknown	AA617405					EST; Unknown	
AA230776	1.00	-1.20	0.86	0.52	1.28	2.33	2.78	0.57	3.29	0.37	thymosin beta 10 (prothymosin beta 10)	AA230776					Structural Protein	
Msa.2614.0	1.00	-1.39	0.50	0.64	1.59	0.53	3.76	0.38	3.28	0.68	properdin factor, complement; Pfc	X12905	properdin (fragment).			X 6.2 cM	Extracellular Protein	
AF017989	1.00	-2.81	-2.56	1.30	0.09	2.39	1.91	0.42	3.28	0.60	stromal cell derived factor 5; Sdf5	AF017989				338.5 cM	Extracellular Protein	
M24509	1.00	1.04	2.36	0.66	2.25	0.67	3.25	0.83	3.27	0.73	ferritin heavy chain; Fth	M24509	ferritin heavy chain (ferritin h subunit).			192.0 cM		
Msa.4744.0	1.00	1.13	2.87	0.83	2.31	1.28	3.00	2.22	3.27	1.91	topoisomerase (DNA) I; TopI	W10047	dna topoisomerase I (ec 5.99.1.2).			292.0 cM		

Accession	1.00	-1.52	0.42	0.73	1.06	2.21	3.37	0.68	3.25	0.38	lysosomal-associated protein transmembrane 5; Laptm5	U29539	lysosomal-associated protein (retinoic acid-inducible c3 protein).	the expression pattern of the gene together with preliminary evidence that the protein interacts with ubiquitin indicates that the protein may have a special functional role during embryogenesis and in adult hematopoietic cells. it		Proteolytic	
AA125580	1.00	-1.07	1.43	0.44	1.46	0.06	3.65	0.56	3.22	0.64	synaptosomal-associated protein, 23kD; Snap23	AA125580			2 61.8 cM		
X93328	1.00	-1.75	0.32	0.79	0.38	1.69	3.03	0.17	3.21	0.44	EGF-like module containing, mucin-like, hormone receptor-like sequence 1; Emr1	X93328	cell surface glycoprotein emr1 precursor (emr1 hormone receptor) (cell surface)	probably involved in cell adhesion within tissues and receptor signalling.	17 34.3 cM	Cell Surface Protein	
Msa.35983.0	1.00	-1.10	-1.46	1.04	0.12	1.54	2.65	0.50	3.19	0.26	secreted phosphoprotein 1; Spp1	AA123395	precursor (bone sialoprotein 1) (minopontin) (early t lymphocyte activation 1 protein) (secreted phosphoprotein 1) (spp-1) (2ar) (calcium oxalate crystal growth inhibitor secretion)	binds tightly to hydroxyapatite. appears to form an integral part of the mineralized matrix. probably important to cell-matrix interaction.	5 56.0 cM	Cytokine	*
Msa.2173.0	1.00	1.16	0.76	0.57	0.37	1.73	3.13	0.44	3.17	0.38	inhibin beta-A; Inhba	X69619	inhibin beta a chain precursor (activin beta-a chain).	inhibin is a gonadal glycopeptide that inhibits the secretion of follitropin by the pituitary gland. on the other hand activin activates the secretion of follitropin. activin is also important in embryonic axial development.	13 10.0 cM	Cytokine	*

# Table 1: "F34E2001"

AF004874	1.00	-1.80	-0.96	0.71	0.93	2.54	3.03	1.07	3.16	0.29	latent transforming growth factor beta binding protein 2; Lbp2	AF004874		human protein is structurally similar to fibrillin. plays a role in bone biology? lbp-2 gene expression in mouse embryos was restricted to cartilage perichondrium and blood vessels, a somewhat surprising result since other lbp genes are expressed	12 D	Unknown	
L38971	1.00	-2.23	-1.09	0.80	1.13	2.99	0.72	1.31	3.15	0.99	integral membrane protein 2; ltm2	L38971	integral membrane protein 2a (c25 protein).		X 37.0 cM		
Msa.64.0	1.00	-1.16	0.10	0.84	0.73	1.75	3.06	0.40	3.15	0.40	collagen binding protein 1; Cbp1	D12907	47 kda heat shock protein precursor (collagen-binding protein 1) (serine protease inhibitor ifi6)	binds specifically to collagen. could be involved as a chaperone in the biosynthetic pathway of collagen		Intracellular Protein	
M31418	1.00	-1.10	1.14	0.90	1.73	2.88	3.24	0.81	3.13	0.18	interferon activated gene 202A, interferon activated gene 202B; Ifi202a, Ifi202b	M31418	interferon-activatable protein 202a (ifi-202a) (interferon-inducible protein p202a)., interferon-activatable protein 202b (ifi-202b) (interferon-inducible protein p202b).	transcriptional activity of several transcription factors, including nf-kappa-b p5 and p65, ap-1, c-fos, c-jun, c2f-1, c2f-4, myod and myogenin. inhibits the transcriptional activity of p53., inhibits the transcriptional activity of c-myc.	1,1 95.2 cM		
AA177300	1.00	-1.63	-1.28	0.98	0.84	2.56	3.22	1.35	3.11	0.45	DNA segment, Chr 13, Abbott 1 expressed; D13Abble	AA177300	seven transmembrane domain protein, upregulated during kidney development.		13 6.0 cM	Cell Surface Protein	
X56304	1.00	-1.02	-2.37	1.63	0.48	2.28	2.63	0.39	3.10	0.34	tenascin C; Tnc	X56304	extracellular matrix glycoprotein expressed in developing brain, mesenchyme, and cartilage, osteoblasts, periosteal and perichondrial cells, and articular surfaces, and is maintained into adult stages in some tissues, notably the		4 32.2 cM	ECM (Matrix Prot)	



AA537404	1.00	-1.18	-0.66	0.85	0.43	1.49	2.74	0.44	2.97	0.34	thymosin beta-10; from rat	AA537404			expressed at relatively high levels in embryonic tissues, and its mrna is abundant in a variety of tumors and tumor cell lines. a major intracellular g-actin binding protein. (a) plays a significant and possibly obligatory role in cell division		Structural Protein	
AA285635	1.00	2.08	-0.32	0.77	3.37	2.34	3.01	1.30	2.95	0.72	ectoplacental cone, invasive trophoblast giant cells, extraembryonic ectoderm and chorion sequence 21; Epos21-pending	AA285635				EST; Unknown		
Msa.8157.0	1.00	-1.28	-0.93	0.86	0.17	1.94	2.89	0.07	2.95	0.33	cathepsin S; Ctss	AA089333			the cathepsins are mammalian lysosomal cysteine proteinases. they play an important role in protein catabolism within the cell, and may be involved in tumor metastasis	3 42.7 cM	Proteolytic	
D50586	1.00	1.00	0.03	0.57	0.22	1.43	3.12	0.85	2.95	0.33	tissue factor pathway inhibitor 2; Tfp2	D50586				6 1.0 cM		
M74149	1.00	-1.31	-1.11	1.25	0.64	1.77	2.40	0.75	2.94	0.38	creatine kinase, brain; Ckb	M74149		creatine kinase, b chain (ec 2.7.3.2) (bck).	reversibly catalyzes the transfer of phosphate between atp and various phosphogens (e.g. creatine phosphate). creatine kinase isoenzymes play a central role in energy transduction in tissues with large, fluctuating energy demands, such as skeletal muscle, heart, brain, and	12 55.0 cM	Metabolic	



# Top of the Foot

Msa.805.0	1.00	1.60	2.03	1.10	2.06	0.82	1.55	0.25	2.94	1.18	immunoglobulin heavy chain 1 (serum IgG2a);immunoglobulin heavy chain 3 (serum IgG2b);immunoglobulin heavy chain 4 (serum IgG1);immunoglobulin heavy chain 6 (heavy chain of IgM); IgH-1,IgH-3,IgH-4,IgH-5	J00475					12 58.0 cM	Hemostasis	
Msa.7614.0	1.00	-1.36	-0.23	0.68	0.48	1.57	4.41	0.21	2.93	0.49	homolog (84%) of human beta-tubulin	W18778						EST: Unknown	
Msa.3176.0	1.00	1.60	0.10	0.64	1.34	0.17	1.78	0.17	2.91	0.37	cathepsin E; Ctse	X97399	cathepsin e precursor (ec 3.4.23.34).	due to its intracellular location and distribution in lymphoid associated tissue, it may have a role in immune function	1 69.1 cM	Proteolytic			
X60367-2	1.00	1.25	-0.64	0.89	1.48	0.40	1.75	0.34	2.91	0.22	retinol binding protein 1, cellular; Rbp1	X60367	retinol-binding protein 1, cellular (mcrbp).	the rbp1 gene encodes crbp, a protein present in a wide variety of adult rat tissues but most abundant in liver and kidney	9 52.0 cM	Regulatory			
AA542220	1.00	1.33	0.43	1.01	2.01	3.11	3.69	1.55	2.90	0.77	TBX1 protein; TBX1	AA542220	tbx1 protein (t-box protein 1) (testis-specific t-box protein) (fragment).	estrogen treatment resulted in a rapid and transient increase in eet-1 messenger ma; steady state levels peaked between 2-3 h, returning to basal levels by 6 h. this increase was not abolished by pretreatment with cycloheximide, indicating		Intracellular Protein			
ab000822	1.00	1.09	1.15	0.61	2.65	1.54	3.02	0.68	2.90	0.52	synaptosomal-associated protein, 23kD; Snap23	AB000822			2 61.8 cM				
ab009287	1.00	-1.10	-0.70	0.66	0.26	1.71	2.69	0.03	2.89	0.42	CD68 antigen; Cd68	AB009287	macrosialin precursor (cd68 antigen).	a.k.a macrosialin --the glycoprotein macrosialin is expressed specifically in murine monocytes and macrophages.	11 39.0 cM	Cell Surface Protein			

# Protein Data Bank

M74227	1.00	-1.62	-1.17	0.88	0.50	1.83	1.58	0.28	2.88	0.15	peptidylprolyl isomerase C; Ppic	M74227	peptidyl-prolyl cis-trans isomerase c (ec 5.2.1.8) (piase) (rotamase) (cyclodilin c).	ppases accelerate the folding of proteins.		Intracellular Protein	
Msa.1629.0	1.00	1.00	0.48	1.03	0.32	1.52	2.16	0.22	2.88	0.26	proteasome (prosome, macropain) subunit, beta type 8 (large multifunctional protease 7); Psmb8	U22031	proteasome component c13 precursor (ec 3.4.99.46) (macropain subunit c13) (multicatalytic endopeptidase complex subunit c13).	the proteasome is a multicatalytic proteinase complex which is characterized by its ability to cleave peptides with arg, phe, tyr, leu, and glu adjacent to the leaving group at neutral or slightly basic ph. the proteasome has an atp-dependent proteolytic activity. this subunit may be involved in	17 18.61 cM	Proteolytic	
X04648	1.00	1.05	-0.62	0.83	0.26	2.21	3.17	0.23	2.87	0.37	Fc receptor, IgG, low affinity IIb; Fcgr2b	X04648	low affinity immunoglobulin gamma fc region receptor ii precursor (fc-gamma rii) (fcrri) (igg fc receptor ii beta) (fc gamma receptor iib) (fcgammariib).	a second low affinity receptor for the fc portion of igg. fc-gammarii and fc-gammarii receptors are identical to low affinity receptor for ige on mouse mast cells and macrophages. fc-gammarii is immunologically	1 92.3 cM	Receptor	
M64086	1.00	-1.36	-3.46	4.25	1.63	3.55	4.80	1.51	2.87	0.36	serine protease inhibitor 2-2; Spi2-2	M64086				Proteolytic	
Msa.27449.0	1.00	1.12	-1.53	0.84	0.19	1.58	2.12	0.37	2.87	0.09	secreted phosphoprotein 1; Spp1	AA066782	osteopontin precursor (bone sialoprotein 1) (minopontin) (early t lymphocyte activation 1 protein) (secreted phosphoprotein 1) (spp-1) (2ar) (calcium oxalate crystal growth inhibitor) (osteocalcin).	binds tightly to hydroxyapatite. appears to form an integral part of the mineralized matrix. probably important to cell-matrix interaction.	5 56.0 cM	ECM (Matrix Prot)	
AA140446	1.00	-1.61	-1.09	0.72	0.32	1.85	4.28	2.43	2.84	0.37	DNA segment, Chr 13, Abbott 1 expressed; D13Abble	AA140446		seven transmembrane domain protein, upregulated during kidney development.	13 6.0 cM	Cell Surface Protein	

AA547057	1.00	1.21	1.69	0.71	1.88	0.13	3.69	0.54	2.83	0.29	ets variant gene 6 (TEL oncogene); ETV6	AA547057	ets-related protein tel (ets translocation variant 6)		6 63.9 cM	Extracellular Protein	
AA259726	1.00	1.02	0.74	0.62	2.33	1.10	3.74	1.63	2.82	0.44	EST; Unknown	AA259726				EST; Unknown	
ET61206	1.00	2.05	1.11	0.76	1.81	0.45	0.70	1.08	2.81	0.31		ET61206				EST; Unknown	
Msa.10497.0	1.00	-4.02	2.16	0.97	0.52	2.77	3.48	2.46	2.79	1.43		W48224					
ET62056	1.00	2.54	-0.61	1.70	1.79	0.33	0.68	1.04	2.78	0.40	immunoglobulin rearranged kappa chain	ET62056				Extracellular Protein	
L06039	1.00	-1.13	0.20	0.74	0.84	2.13	2.78	1.03	2.77	0.13	platelet/endothelial cell adhesion molecule; Pecam	L06039	platelet endothelial cell adhesion molecule precursor (pecam-1) (cd31 antigen).	functions in cell-cell adhesion...expression in lymphocytes transmigration the endothelial cell lining...the function of pecam in the emigration process is not solely to bring leukocytes into contact with the vascular endothelium	6 31.5 cM	Hemostasis	
U90355	1.00	-1.22	-1.48	1.29	0.21	1.62	2.12	0.27	2.77	0.25	fascin homolog 1 (actin bundling protein, Strongylocentrotus purpuratus); Fascin	U90355	fascin.	organizes filamentous actin into bundles with a minimum of 4:1:1 actin/fascin ratio.	5 86.0 cM	Structural Protein	
AA255186	1.00	-1.71	0.71	0.70	0.32	2.47	3.26	0.66	2.76	0.24	numatrin; Ctsd	AA255186		lysosomal cysteine proteinase	3 42.7 cM	Proteolytic	
AA030649	1.00	-1.29	-0.57	0.54	0.18	2.27	1.99	0.28	2.76	0.51	procollagen, type V, alpha 1; Col5a1	AA030649		type v collagen is a member of group i collagen (fibrillar forming collagen). collagen v is expressed in connective tissue in close contact with the vascular basement membrane in bone, skin, cartilage, tendon,	2 18.0 cM	ECM (Matrix Prot)	
Msa.544.0	1.00	-2.55	-3.78	2.77	-0.05	1.74	1.98	0.15	2.75	0.27	procollagen, type V, alpha 2; Col5a2	L02918				ECM (Matrix Prot)	
AA690738	1.00	-1.06	0.68	0.56	1.54	0.10	2.40	0.32	2.74	0.47	EST; Unknown	AA690738				EST; Unknown	
AA711271	1.00	-1.70	-0.60	0.75	0.81	2.07	3.05	1.23	2.73	0.39	EST; Unknown	AA711271				EST; Unknown	

\*



# Table 2001

M14215	1.00	-1.13	-0.86	1.07	0.23	1.57	2.64	0.30	2.61	0.53	Fc receptor, IgG, low affinity III; Fcγ3	M14215	low affinity immunoglobulin gamma fc region receptor iii precursor (igg fc receptor iii) (fc-γRIIIb)	receptor for the fc region of complexed immunoglobulins gamma. low affinity receptor.	192.3 cM	Receptor	
AA212971	1.00	-2.70	0.35	0.65	0.63	1.84	2.80	0.19	2.59	0.23	lipopolysaccharide binding protein; Lbp	AA212971	lipopolysaccharide-binding protein precursor (lbp)	binds to the lipid moiety of bacterial lipopolysaccharides (lps), a glycolipid present in the outer membrane of all gram-negative bacteria. the lbp/lps complex seems to interact with the cell wall.	283.0 cM		
J04694	1.00	-1.84	-0.92	0.75	0.39	1.77	2.03	0.40	2.58	0.14	procollagen, type IV, alpha 1; Col4a1	J04694	collagen alpha 1(iv) chain precursor.	type iv collagen forms the collagenous matrix of the basement membrane, an extracellular lamina closely applied to the basal surface of epithelium and also occurring in other tissues.	85.0 cM	ECM (Matrix Prot)	
U55060	1.00	-1.11	-0.14	0.95	0.46	2.02	2.12	0.36	2.58	0.19	lectin, galactose binding, soluble 9; Legals9	U55060	galectin-9.	binds galactosides. may play a role in thymocyte-epithelial interactions relevant to the biology of the thymus.			
J05020	1.00	-1.25	0.10	0.58	0.47	1.92	2.51	0.11	2.57	0.22	Fc receptor, IgE, high affinity I, gamma polypeptide; Fcε1g	J05020	high affinity immunoglobulin epsilon receptor gamma-subunit precursor (fcεr1)	the high affinity ige binding receptor (fcεpsilon1r) is found exclusively on mast cells and basophils.	193.3 cM	Cell Surface Protein	
AA023914	1.00	2.46	0.98	0.71	1.88	0.37	2.22	0.36	2.56	0.17		AA023914	epsilon fc receptor, gamma-subunit (fc-εgamma)				

# Table 1

U06119	1.00	-1.00	0.51	0.62	1.60	0.49	2.18	0.08	2.56	0.29	cathepsin H; Cish	U06119	cathepsin h precursor (ec 3.4.22.16) (cathepsin b3) (cathepsin ba).	activation of macrophages by gamma-interferon induces expression of major histocompatibility complex (mhc) class ii genes. an increase in cathepsin h, encoded in the mouse by cish, is also induced by gamma-interferon and	9 50.0 cM	Proteolytic	
D38162	1.00	-2.75	-1.55	0.62	-0.14	1.74	0.58	1.10	2.54	0.31	procollagen, type XI, alpha 1; Col11a1	D38162	collagen alpha 1(x1) chain precursor.	may play an important role in fibrillogenesis by controlling lateral growth of collagen ii fibrils.	3 53.1 cM	ECM (Matrix Prot)	
AA108054	1.00	-1.40	-0.41	0.50	1.29	0.21	1.78	0.28	2.53	0.24	serine protease inhibitor 6; Spif6	AA108054			13 16.0 cM		
U56819	1.00	-1.28	0.64	0.60	0.83	1.98	4.27	0.29	2.53	0.17	chemokine (C-C) receptor 2; Cnkr2	U56819	c-c chemokine receptor type 2 (c-c ckr-2) (cc-ckr-2) (ccr-2) (ccr2) (je/fic receptor) (mcp-1 receptor).	receptor for the mcp-1 (je), mcp-3 (fic) and mcp-5 chemokines. transduces a signal by increasing the intracellular calcium ions level	9 72.0 cM		
Msa.16995.0	1.00	-1.11	-2.58	2.64	-0.12	1.95	3.20	0.17	2.52	0.46	arachidonate 5-lipoxygenase activating protein	W83564		seems to be required for the activation of 5-lo (5-lipoxygenase). flap could play an essential role in the transfer of arachidonic acid to 5-lo. flap binds to mk-886, a compound that blocks the biosynthesis of leukotrienes.		Intracellular Protein	
Msa.88.0	1.00	-2.30	-4.15	2.92	0.09	2.23	1.91	0.28	2.52	0.21	osteoblast specific factor 2; OSF-2	D13664		preferentially expressed in periosteum and periodontal ligament. involved in cell adhesion, highly homologous to beta-actin, a molecule induced by transforming growth factor beta (tgf-beta) that promotes the		Extracellular Protein	

[illegible]

ET62844	1.00	-1.11	0.55	0.84	1.46	0.45	2.77	0.34	2.52	0.33	paired-Ig-like receptor A10, paired-Ig-like receptor A6; PirA10, PirA6	ET62844	7	7	Receptor
M33203	1.00	1.33	-0.49	1.58	1.69	2.85	3.74	1.06	2.50	0.63	heme oxygenase (decycling) 1; Hmox1	M33203	8 C1	heme oxygenase catalyzes the degradation of heme into biliverdin, carbon monoxide, and iron. two forms of this enzyme, heme oxygenase-1 and -2, have been identified; only heme oxygenase-1 is subject to induction by heme, <del>model ligand and substrate</del>	Intracellular Protein
D17630	1.00	-1.27	0.33	0.56	0.10	1.13	2.98	0.37	2.49	1.24	chemokine (C-X-C) receptor 2; Cxcr2	D17630	1 40.0 cM	high affinity interleukin-8 receptor b (il-8r b) (cxcr-2) (gro/mgsa receptor).	
U41765	1.00	-1.40	0.41	0.73	0.60	1.70	2.85	0.58	2.48	0.16	a disintegrin and metalloproteinase domain 9 (meltrin family); Adam9	U41765	8 8.0 cM	receptor binds to il-8 with a high affinity and to gro/mgsa and map-2 also with a high	
Msa.1376.0	1.00	1.08	-2.10	1.22	0.19	1.46	1.88	0.21	2.48	0.09	phosphoprotein 1; Spp1	X16151	5 56.0 cM	binds tightly to hydroxyapatite. appears to form an integral part of the mineralized matrix. probably important to cell-matrix interaction.	Cytokine

U92437	1.00	-1.85	1.71	0.67	2.06	0.03	2.72	0.35	2.48	0.28	phosphatase and tensin homolog; Pten	U92437	protein-tyrosine phosphatase pten (ec 3.1.3.48) (mutated in multiple advanced cancers)	potential tumor suppressor. active as a phosphatase on tyrosine, serine and threonine residues. no match on blast search 1/99.	19 24.5 cM		
AA667371	1.00	-2.99	-1.56	0.83	-0.40	2.70	0.68	0.93	2.42	0.25	Unknown	AA667371	growth arrest and DNA-damage- inducible protein Gadd45g	plays an important role in negative growth control, including both growth suppression and apoptosis.		EST; Unknown Regulatory	
Msa.7498.0	1.00	1.38	-0.01	1.13	0.49	1.77	2.90	0.20	2.41	0.37	growth arrest and DNA-damage- inducible protein Gadd45g	AA138777	growth arrest and DNA-damage- inducible protein gadd45 gamma (cytokine responsive protein erf).				
S74567	1.00	-1.41	3.30	0.41	2.84	1.39	2.88	0.80	2.39	1.21	avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog; Maf	S74567	transcription factor maf2 (proto- oncogene c-maf).	the c-maf interaction site was mapped to the sequence 5'- [g]g[gc]n[gt]nctcag- 3' in the 17 promoter. it may interact with additional basic-zipper proteins that determine a subtype of maf-responsive element binding.	8 61.0 cM		
AA238081	1.00	-1.19	-1.01	1.19	0.78	2.13	2.04	0.37	2.39	0.24	complement 1, r subcomponent; C1r	AA238081			6		
W53443	1.00	1.39	-1.66	1.86	0.32	1.35	1.74	0.34	2.38	0.13	GENESEQ:V34267 Human secreted protein gene 58 clone HSSEP68.	W53443		also a good match to human clone 2491 (af131781) (both are 89%)		EST; Unknown	
L28177	1.00	1.22	-0.67	1.07	0.03	1.44	5.51	0.19	2.36	0.44	DNA-damage inducible transcript 1; Ddit1	L28177	growth arrest and DNA-damage- inducible protein gadd45.	binds to proliferating cell nuclear antigen. might affect pten interaction with some cdk (cell division protein kinase) complexes; stimulates DNA excision repair in vitro and inhibits entry of cells into S phase.	3 70.5 cM	Intracellular Protein	
Msa.928.0	1.00	-1.07	-1.99	1.35	0.25	1.47	1.88	0.09	2.35	0.18	myristoylated alanine rich protein kinase C substrate; Macs	M60474	myristoylated alanine-rich c- kinase substrate (marcks).	marcks is the most prominent cellular substrate for protein kinase c. this protein binds calmodulin, actin, and synapsin. marcks is a filamentous (f) actin cross-linking protein	10 22.0 cM	Structural Protein	



# Table 200

AA475111	1.00	-1.27	1.20	0.45	1.54	0.12	2.49	0.30	2.31	0.19	heterogeneous nuclear ribonucleoprotein D-EST; Unknown	AA475111							
AA536849	1.00	-1.97	0.31	0.73	3.28	1.85	2.32	0.71	2.31	0.51	EST; Unknown	AA536849							
C81524	1.00	-1.20	2.02	0.85	1.09	2.55	1.96	1.84	2.31	1.29		C81524							
AA170245	1.00	1.08	0.79	0.45	0.60	1.69	2.32	0.10	2.30	0.18		AA170245							
AF013262	1.00	-2.69	-0.93	0.72	1.19	2.74	2.01	0.60	2.30	0.72	lumican; Lum	AF013262	lumican precursor (lum) (keratan sulfate proteoglycan).	leucine-rich proteoglycan with keratan sulfate side chains, a major component of cornea, dermal, and muscle connective tissues. regulation of collagen assembly into fibrils in various connective tissues. lumican is necessary in the development of the cornea.	10 61.0 cM	ECM (Matrix Prot)			
AF020313	1.00	-1.73	0.47	0.68	1.07	2.46	3.40	1.07	2.30	0.16	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein; Apbb1ip-1	AF020313					Extracellular Protein		
Msa.22488.0	1.00	1.08	-1.88	1.54	0.27	2.19	2.75	0.57	2.30	0.22	cathepsin S; Ctss	AA146437		the cathepsins are mammalian lysosomal cysteine proteinases. they play an important role in protein catabolism within the cell, and may be involved in tumor metastasis	3 42.7 cM	Proteolytic			
AF004666	1.00	1.09	0.15	0.48	0.11	1.17	2.68	0.32	2.27	0.40	solute carrier family 8 (sodium/calcium exchanger), member 1; Slc8a1	AF004666	sodium/calcium exchanger 1 precursor (na+/ca2+ exchange protein 1).	rapidly transports ca2+ during excitation-contraction coupling. ca(2+) is extruded from the cell during relaxation so as to prevent overloading of intracellular stores	17 48.0 cM				
Msa.1171.0	1.00	0.63	-0.50	0.61	0.72	2.71	-0.69	1.03	2.27	2.79	keratin-associated protein 5-4; Krtap5-4	M37760							

# Protein Data Bank

Accession	Residue	1.00	-1.85	-0.89	1.02	0.31	1.63	2.14	0.05	2.25	0.17	lectin, galactose binding, soluble I; LgalSI	W13002	galectin-1 (beta-galactoside-binding lectin I-14-I) (lactose-binding lectin I) (s-lac lectin I) (galapin) (14 kda lectin).	postimplantation, lgalSI is expressed in somite myotomes, suggesting a role in muscle development. this protein binds beta-galactoside. its physiological function is not yet known. it may act as an autocrine negative growth factor that controls a cysteine endopeptidase. legumain was found in all mouse tissues examined, but was particularly abundant in kidney and placenta. the distribution in subcellular fractions of mouse and rat kidney showed a	15 44.9 cM	Other	
Msa.5619.0		1.00	-1.16	-3.48	2.53	-0.07	2.03	2.48	0.33	2.22	0.22	protease, cysteine, I; PrscI	AA000961			Proteolytic		
AA119603		1.00	1.13	1.06	0.58	1.58	0.16	2.17	0.13	2.22	0.30	L1 repeat, Tf subfamily, member 14.L1 repeat, Tf subfamily, member 29; LIMd-	AA119603				EST; Unknown	
D84391		1.00	-1.58	1.92	0.91	2.05	0.87	1.83	1.73	2.21	1.32		D84391					
X16874		1.00	-1.38	-1.89	2.31	0.25	1.88	2.10	0.00	2.17	0.18	complement component 1, q subcomponent, beta polypeptide; C1qb	X16874	complement c1q subcomponent, b chain precursor.	the primary humoral mediator of antigen-antibody reactions is the complement (c) system.	4 66.1 cM	Hemostasis	
AF022992		1.00	4.47	1.39	0.28	0.21	1.33	1.55	1.17	2.16	0.30	period homolog (Drosophila); Per	AF022992	per-hexamer repeat protein 5..period circadian protein 1 (circadian pacemaker protein fruit) (mncr) (m-	circadian regulator that may act as a transcription factor. behaves as a negative element in circadian transcriptional loop.	11 B	Other	

# FOREF "T94E20"

U69135		1.00	1.15	-7.17	7.77	1.42	0.28	2.76	0.71	2.16	0.11	uncoupling protein 2, mitochondrial; Ucp2	U69135	mitochondrial uncoupling protein 2 (ucp 2) (ucph).	ucp are mitochondrial transporter proteins that create proton leaks across the inner mitochondrial membrane, thus uncoupling oxidative phosphorylation from atp synthesis. as a result, energy is dissipated in the form of heat.	750.0 cM	Intracellular Protein	
Msa.4530.0		1.00	1.34	0.13	0.56	1.33	0.21	2.22	0.10	2.16	0.41	EST; region of homology to GENESEQN:Z77537 Human ovarian tumor cDNA library derived EST fragment.88	AA106931				EST; Unknown	
Msa.34975.0		1.00	3.11	1.82	0.58	1.92	0.83	2.57	0.42	2.14	0.22	eukaryotic translation initiation factor 2, subunit 3, structural gene Y-linked; Eif2s3y	AA118716	eukaryotic translation initiation factor 2 gamma subunit y-linked (eif2-gamma y).	eif-2 functions in the early steps of protein synthesis by forming a ternary complex with gtp and initiator trna. this complex binds to a 4s ribosomal subunit, followed by mrna binding to form a 43s preinitiation complex. junction of the 6s ribosomal subunit to form the 8s initiation complex is preceded by hydrolysis of the gtp bound to eif-2 and release of an eif-2-gdp binary complex. in order for eif-2 to recycle and catalyze another round of initiation, the gdp bound to eif-2 must exchange with gtp by way of a reaction catalyzed by eif-2b (by	Y	Regulatory	
AA616077		1.00	-1.88	-0.15	0.53	1.56	0.52	2.53	0.27	2.13	0.17		AA616077				EST; Unknown	
AA607513		1.00	-3.27	-3.57	2.01	-0.15	2.43	0.84	0.96	2.13	0.33	Unknown	AA607513		blast analysis of 1299.		EST; Unknown	
ET62894		1.00	-3.02	0.12	0.95	0.03	1.39	1.03	1.20	2.09	0.16		ET62894		blast analysis of 5/		EST; Unknown	

U31993	1.00	1.00	-0.75	0.59	0.42	1.89	2.35	0.25	2.08	0.24	interleukin 17 receptor; IL17r	U31993				655.2 cM	Receptor		
Msa.9251.0	1.00	-1.29	-1.33	0.91	0.29	1.90	2.56	0.10	2.05	0.37	neutrophil cytosolic factor 2; Ncf2	AA050149				176.1 cM	Intracellular Protein		
Msa.978.0	1.00	-1.00	-1.30	1.35	0.07	1.36	2.07	0.05	2.04	0.24	moesin; Msn	M86390	moesin (membrane-organizing extension spike protein).	thought to work as cross-linkers between plasma membranes and actin-based cytoskeletons. these molecules are involved not only in cytoskeletal organization but also in signal transduction.	X		Cell Surface Protein		
AA474881	1.00	-1.06	1.37	0.61	1.85	0.05	2.66	0.28	2.01	0.20	DNA segment, Chr 1, Wayne State University 40, expressed.	AA474881			117.0 cM				
AA204590	1.00	-1.39	0.50	0.54	0.11	1.23	3.51	0.74	2.01	0.31	EST; Unknown	AA204590					EST; Unknown		
AA691533	1.00	-7.45	-1.37	0.88	0.56	2.15	0.50	0.96	2.00	0.50		AA691533					EST; Unknown		
Msa.17862.0	1.00	-6.92	-1.98	0.96	-0.02	1.49	1.85	0.27	1.99	0.12	lysyl oxidase-like; Loxl	W98413				933.0 cM			
Msa.29217.0	1.00	-3.11	-1.61	3.81	1.65	0.59	2.80	0.79	1.96	0.30	actin, beta, cytoplasmic	AA079937					Structural Protein		
Msa.24381.0	1.00	-2.44	0.70	0.66	0.52	1.55	2.40	0.55	1.92	0.35	damage specific DNA binding protein 1 (127 kDa); Ddb1	W42399				195.0 cM	Other		
X57337	1.00	-2.45	-1.87	0.89	-0.11	1.76	1.39	0.13	1.91	0.19	procollagen C-proteinase enhancer protein; Pce	X57337	procollagen C-proteinase enhancer protein precursor (pce) (type I procollagen co-terminal proteinase enhancer) (type I procollagen C-proteinase enhancer)	a glycoprotein that potentiates enzymatic cleavage of the type I procollagen C-propeptide by bone morphogenetic protein 1 (bmp-1)	578.0 cM	Extracellular Protein			
Msa.2924.0	1.00	-1.06	-0.71	0.56	0.35	1.36	2.66	0.30	1.91	0.27	superoxide dismutase 3, extracellular; Sod3	X84940	superoxide dismutase [cu-zn] precursor (ec 1.15.1.1) (ec-sod)	destroys radicals which are normally produced within the cells and are toxic to biological systems.	531.0 cM				
AA608277	1.00	1.72	0.73	0.50	1.21	0.03	2.36	0.18	1.91	0.42		AA608277							

# Table 1

U75530	1.00	-1.41	3.24	1.00	0.89	2.65	1.99	3.07	1.90	1.73	eukaryotic translation initiation factor 4E binding protein 2; Eif4ebp2	U75530			10 32.0 cM		
M91380	1.00	-2.56	-2.42	1.30	-0.27	1.66	1.64	0.21	1.89	0.10	foliostatin-like; Fsl	M91380	foliostatin-related protein precursor (tgf-beta-inducible protein tsc-36).	tgfb responsive gene cloned from an osteoblastic cell line. encodes a protein of 35 kda. the amino acid sequence of tsc-36 protein was found to be similar to foliostatin, an activin-binding protein, also similar to the secreted	16 27.3 cM	Extracellular Protein	
Msa.21961.0	1.00	-2.48	-0.32	0.79	-0.12	1.13	1.58	0.25	1.89	0.26	EST; Unknown	AA030421		est		EST; Unknown	
Z31334	1.00	-2.57	-3.02	1.52	-0.47	1.96	0.49	0.81	1.84	0.12	procollagen, type I, alpha 2; Cola2	Z31334	collagen alpha 2(i) chain precursor.	type i collagen, the commonest form, is a fibrillar collagen, along with types ii, iii, v. and xi.	6 0.68 cM	ECM (Matrix Prot)	
AA176016	1.00	-2.13	0.89	0.73	1.69	0.05	2.43	0.32	1.82	0.19		AA176016					
AA510381	1.00	1.29	1.66	0.99	0.08	1.75	1.14	1.51	1.82	1.19		AA510381					
AA146539	1.00	-1.05	1.80	0.52	1.91	0.05	2.13	0.31	1.78	0.07	EGF-like repeats and discordin 1-like domains 3; Edil3	AA146539					
Msa.2536.0	1.00	2.69	-0.19	0.81	1.43	0.08	1.88	0.57	1.74	0.20	extracellular proteinase inhibitor; Expi	X93037	wdm1 protein precursor.	could have proteinase inhibiting capacity.			
D78188	1.00	-2.03	0.04	0.66	0.34	2.02	1.82	0.41	1.74	0.26	granule cell differentiation protein; Gcdp	D78188	myotrophin (v-1 protein) (granule cell differentiation protein).	potential role in cerebellar morphogenesis. may function in differentiation of cerebellar neurons, particularly of granule cells.			
X93037	1.00	3.54	-0.36	0.70	1.60	0.26	1.81	0.49	1.73	0.20	extracellular proteinase inhibitor; Expi	X93037	wdm1 protein precursor.	could have proteinase inhibiting capacity.			

# Protein Feature

W45778	1.00	4.09	-1.35	1.46	0.39	2.02	0.59	0.83	1.73	0.38	von Willebrand Factor; vWF; homolog	W45778			vwf binds to and stabilizes coagulation factor viii (c18) and also mediates interaction between platelets and the blood vessel wall. expressed in endothelial megakaryocytes, stored in platelets alpha-granules and within the weibel-		Hemostasis	
Msa.2220.0	1.00	-2.16	0.07	0.79	0.03	1.17	0.67	0.91	1.71	0.21	procollagen, type I, alpha 2; Cola2	X58251	collagen alpha 2(i) chain precursor.		forms the fibrils of tendon, ligaments and bones. in bones the fibrils are mineralized with calcium hydroxapatite.	6 0.68 cM	ECM (Matrix Prot)	
V01527	1.00	-2.25	-0.93	1.01	0.19	1.46	1.95	0.04	1.71	0.21	histocompatibility class II antigen A, beta 1; H2-Abl	V01527	h-2 class ii histocompatibility antigen, a-d beta chain precursor.		this is a class ii antigen, i-a-beta.	17 18.64 cM	Cell Surface Protein	
U79144	1.00	-5.09	-3.07	1.98	-0.09	1.71	1.50	0.17	1.70	0.21	lysyl oxidase-like; Loxl	U79144			homolog of lysyl oxidase which maps to chr 18	9 33.0 cM	EST; Unknown	
U64450	1.00	-0.37	1.53	0.84	0.23	1.85	2.57	0.59	1.68	0.63	nucleoplasmin 3; Npm3	U64450			aka nub1 -- encodes a protein related to the nuclear chaperone phosphoproteins, nucleoplasmin and nucleophosmin	19 45.0 cM	Regulatory	
U11541	1.00	-5.90	-32.12	30.53	-0.45	1.59	-2.26	1.89	1.68	0.31	bone gamma carboxyglutamate protein 1, bone gamma-carboxyglutamate protein 2, bone gamma-carboxyglutamate protein, related sequence 1; Bglap-rs1, Bglap1, Bglap2	U11541	osteocalcin precursor (gamma-carboxyglutamic acid-containing protein) (bone gla-protein) (bglp), osteocalcin-related protein precursor (oc-x) (nephrocalcin).		a.k.a as osteocalcin-related protein. bglap-rs1, is a related sequence which may not be transcribed. it is claimed to resemble, in structure and expression pattern, nephrocalcin, a calcium-binding protein involved in bone metabolism	3 42.6 cM	ECM (Matrix Prot)	

# Table 1

D50460	1.00	-3.16	-1.78	0.97	0.21	1.47	0.41	0.87	1.67	0.15	stromal cell derived factor 3; Sdf3	D50460	pigment epithelium-derived factor precursor (pdf) (stromal cell-derived factor 3) (sdf-3).	a.k.a pigment epithelium-derived factor -- a member of the serine protease inhibitor (serpin) superfamily, promotes survival and/or differentiation of rat cerebellar granule neurons and human retinoblastoma cells in vitro. no inhibitory activity.		Cytokine
C76162	1.00	-2.16	0.93	0.55	1.90	0.72	1.59	0.29	1.66	0.22		C76162				
Msa.27482.0	1.00	-2.98	-0.34	0.93	-0.02	1.68	0.79	0.95	1.63	0.09	DNA segment, Chr 10, Johns Hopkins University 81 expressed; D10H11.81e	AA139094			10 41.7 cM	
X65582	1.00	-2.34	-2.58	0.91	-0.22	1.62	0.31	0.86	1.63	0.20	procollagen, type VI, alpha 2; Col6a2	X65582	collagen alpha 2(vi) chain precursor.	collagen vi acts as a cell-binding protein.	10 41.1 cM	ECM (Matrix Prot)
X58251	1.00	-2.11	-0.18	0.74	0.01	1.14	0.61	0.89	1.62	0.20	procollagen, type I, alpha 2; Cola2	X58251	collagen alpha 2(i) chain precursor.	forms the fibrils of tendon, ligaments and bones. in bones the fibrils are mineralized with calcium hydroxvanilate	6 0.68 cM	ECM (Matrix Prot)
Msa.22727.0	1.00	-2.67	-0.62	2.27	0.42	1.67	1.45	1.31	1.61	0.93	melanoma X-actin; Actx	AA038134				Structural Protein
X66405	1.00	-2.18	-3.12	1.32	-0.39	1.72	-0.54	0.85	1.53	0.22	procollagen, type VI, alpha 1; Col6a1	X66405	collagen alpha 1(vi) chain precursor.	collagen vi acts as a cell-binding protein.	10 41.1 cM	ECM (Matrix Prot)
AF022256	1.00	-3.92	-1.46	0.47	-0.36	1.65	-1.65	1.42	1.49	0.18	keratocan; Kera	AF022256		keratan sulfate proteoglycans (kspgs) play a pivotal role in the development and maintenance of corneal transparency. keratocan, lumican, and mimecan (osteoglycin) are the major kerans in	10 61.0 cM	ECM (Matrix Prot)
Msa.22485.0	1.00	-2.42	-0.72	0.53	1.18	0.18	1.79	0.13	1.49	0.07		AA035834				

Msa.2851.0	1.00	-2.52	-4.32	2.71	-0.35	1.82	1.71	0.13	1.46	0.14	lipopolysaccharide binding protein; Lbp	X99347	lipopolysaccharide-binding protein precursor (lbp).	binds to the lipid moiety of bacterial lipopolysaccharides (lps), a glycolipid present in the outer membrane of all gram-negative bacteria. the lbp/lps complex seems to interact with the cell receptor.	2 83.0 cM		
Msa.117.0	1.00	-2.41	-1.85	0.94	-0.06	1.16	1.28	0.10	1.42	0.08	procollagen, type I, alpha 1; Col1a1	U08020	collagen alpha 1(i) chain precursor.	type i collagen is a member of group i collagen (fibrillar forming collagen).	11 56.0 cM	ECM (Matrix Prot)	
Msa.3557.0	1.00	-2.19	-2.73	1.67	-0.28	1.56	-0.45	0.87	1.40	0.19	stromal cell derived factor 3; Sdf3	W08269	pigment epithelium-derived factor precursor (pdf) (stromal cell-derived factor 3) (sdf-3).	neurotrophic protein; induces extensive neuronal differentiation in retinoblastoma cells. as it does not undergo the s (stressed) to r (relaxed) conformational transition characteristic of active serpins, it exhibits no serine protease		Cytokine	
L29454	1.00	-2.97	-2.34	0.83	-0.28	1.51	0.42	0.76	1.40	0.16	fibrillin 1; Fbn1	L29454	fibrillin 1 precursor.	structural component of connective tissue microfibrils that binds calcium. fibrillin-1-containing microfibrils provide long-term force bearing structural support.	2 71.0 cM		
AA689977	1.00	-2.14	-0.71	1.22	0.22	1.67	1.16	1.17	1.38	0.10	mini chromosome maintenance deficient 6 (S. cerevisiae); Mcm6	AA689977	dna replication licensing factor mem6 (mis5 homolog).	may be involved in the control of a single round of dna replication during s phase. binds to chromatin during gl and detach from it during s phase as if it licenses the chromatin to replicate.			



# Table 1

M18194	1.00	-2.55	-1.79	0.59	0.17	1.34	0.50	0.78	1.36	0.09	fibronectin 1; Fn1	M18194	fibronectin precursor (fn) (fragments).	a glycoprotein that interacts with a variety of cells through both integrin and non-integrin receptors. encoded by a single gene, but alternative splicing of pre-mrna allows formation of multiple isoforms with critical roles in cell adhesion	136.1 cM	Extracellular Protein	
AA285530	1.00	-2.38	-0.40	0.60	-1.07	0.02	0.66	0.94	1.35	0.14		AA285530					
Msa.10146.0	1.00	3.59	-1.35	1.51	0.33	2.24	1.37	0.24	1.31	0.14	vWF; human	AA168633				Hemostasis	
X56602	1.00	-7.23	-2.12	0.76	-5.94	0.81	-1.36	0.13	1.25	1.56	interferon-stimulated protein (15 kDa); Isg15	X56602	ubiquitin cross-reactive protein (interferon-stimulated protein 15)			Cytokine	
Msa.419.0	1.00	16.53	1.33	1.41	-1.51	0.36	-0.88	1.00	1.09	1.75	aminolevulinic acid synthase 2, erythroid; Alas2	M63244	5-aminolevulinic acid synthase, erythroid-specific, mitochondrial precursor (ec 2.3.1.37) (delta-aminolevulinat synthase) (Alas2)	alas, though synthesized on cytoplasmic ribosomes, functions in mitochondria...alas2 encodes the erythrocyte-specific isoform involved in heme biosynthesis	X 63.0 cM	Intracellular Protein	
U08020	1.00	-3.63	-2.35	1.03	0.52	2.00	1.42	0.36	1.07	0.81	procollagen, type I, alpha 1; Col1a1	U08020	collagen alpha 1(i) chain precursor.	type I collagen is a member of group I collagen (fibrillar forming collagen).	11 56.0 cM	ECM (Matrix Prot)	
AA289002	1.00	2.49	-0.24	0.54	-1.32	0.24	-0.42	1.25	1.03	0.69		AA289002				EST; Unknown	
AA684083	1.00	-0.55	0.43	0.57	-0.10	1.37	0.95	0.64	0.99	0.47		AA684083					
Msa.29141.0	1.00	-2.49	0.35	0.77	-0.06	1.40	0.94	1.18	0.96	0.67	myosin Ic; Myolic	AA073795			11 44.13 cM		
Msa.17336.0	1.00	-2.35	0.72	0.79	0.14	1.33	0.88	1.00	0.94	0.70	melanoma X-actin; Actx	W89940		cells derived from the murine b16 melanoma express a third actin which has been designated melanoma x-actin. comparison between x-actin and i-actin structures indicate that x-actin is inherited by a different locus.		Structural Protein	
AA185262	1.00	2.41	-0.69	0.73	-0.01	1.41	1.73	1.87	0.89	0.79	EST; Unknown	AA185262				EST; Unknown	

# Table 1: The sequence logo

Msa.17592.0	1.00	-2.77	-0.35	0.83	-0.30	1.33	1.52	0.24	0.86	0.65	W96831								
Msa.29918.0	1.00	-2.55	0.41	1.16	-0.02	1.09	1.29	1.17	0.85	0.64	AA087943	melanoma X-actin; Actin							
AA396357	1.00	2.43	-2.33	2.31	0.23	1.34	0.26	0.80	0.71	0.59	AA396357	ubiquitin-conjugating enzyme E2H; Ubc2h						6.65 cM	
U77460	1.00	1.01	-1.80	0.64	-0.72	2.22	3.58	0.80	0.70	0.59	U77460	complement component 3a receptor 1; C3ar1	c3a anaphylatoxin chemotactic receptor (c3a-r) (c3ar) (complement component 3a receptor 1)	aka: anaphylatoxin c3a receptor, a g-protein coupled receptor	6 FI			Hemostasis	
Msa.4113.0	1.00	3.13	-1.07	2.02	0.00	2.06	-0.43	1.72	0.69	0.79	AA050733	glucocorticoid-induced leucine zipper; Gilz		expressed in normal lymphocytes from thymus, spleen, and lymph nodes, low or no expression detected in other nonlymphoid tissues, including brain, kidney, and liver. selectively protects t cells from apoptosis induced by treatment with anti-cd				Signal Transduction	
AA222661	1.00	-2.11	-0.06	0.66	-0.09	1.30	-0.44	1.04	0.64	0.61	AA222661								
AA530782	1.00	1.12	-4.81	4.02	-0.29	1.45	-1.23	1.08	0.58	1.24	AA530782	keratin complex-1, gene C29; Krt1-c29					11 57.85 cM		
AF033031	1.00	-0.44	0.93	0.44	0.13	1.15	1.66	1.07	0.56	0.69	AF033031	solute carrier family 27 (fatty acid transporter), member 2; Slc27a2	very-long-chain acyl coa synthetase (ec 6.2.1.-) (very-long-chain- fatty-acid-coa						
X03986	1.00	1.33	-5.21	1.97	-3.07	1.60	0.63	0.84	0.55	0.56	X03986	acetylcholine receptor alpha; Achr	acetylcholine receptor protein, alpha chain precursor.	the alpha, beta, gamma, and delta subunits of the muscle nicotinic acetylcholine receptor, each encoded by its own locus, are assembled into a pentamer of 2 alpha units and one each of the beta, gamma, and delta	2 43.0 cM			Receptor	
AA611341	1.00	1.31	-2.30	1.59	-0.58	5.09	-3.37	0.47	0.54	1.43	AA611341	keratin complex-1, gene C29; Krt1-c29					11 57.85 cM		
AA240803	1.00	4.90	0.13	0.59	-0.01	2.00	3.35	4.03	0.48	1.55	AA240803	Unknown, No hits							EST; Unknown
AB007848	1.00	-2.59	-1.24	0.53	0.22	1.88	-0.61	1.14	0.39	0.87	AB007848	osteomodulin; Omd		a novel bone matrix protein.					ECM (Matrix Prot)

\*

# Table 3

AA426892	1.00	-2.91	-2.01	0.99	0.18	2.47	-0.02	1.21	0.28	1.23	plasminogen activator, tissue; Plaf	AA426892	tissue-type plasminogen activator precursor (ec 3.4.21.68) (tpa) (t-pa) (t-plasminogen activator).	converts the abundant, but inactive, zymogen plasminogen to plasmin by hydrolyzing a single arg-val bond in plasminogen. by controlling plasmin-mediated proteolysis, it plays an important role in tissue remodeling and degradation, in cell migration and many other	8 9.0 cM		
U16175	1.00	-2.81	-2.68	1.32	-1.31	0.31	-0.68	0.98	0.11	0.73	hypothetical protein, mucin 1, transmembrane, thrombospondin 3; LOC54129, Muc 1, Thbs3	U16175	mucin 1 precursor (polymorphic epithelial mucin) (pent) (episialin), thrombospondin 3 precursor.	a secreted glycoprotein member of the class of adhesive proteins. protein appears to have specialized functions in cell growth. thbs3 gene differs markedly from thbs1 and thbs2, both in structure and	3.3 42.6 cM, 3 44.8 cM	Extracellular Protein	
X14194	1.00	-1.05	-2.25	0.71	-0.99	2.19	-0.73	0.96	0.03	0.77	midogen 1; Nid1	X14194			13 7.0 cM		
Msa.18310.0	1.00	-2.23	0.10	1.07	0.05	1.53	-0.59	0.93	-0.05	0.74	ATP citrate-lyase	AA000410		atp citrate-lyase is the primary enzyme responsible for the synthesis of cytosolic acetyl-coa in many tissues. strongly expressed in liver and adrenal, moderate levels were found in lung, brain, and large intestine. of importance in		Metabolic	

# Table 200

Msa.18226.0	1.00	-2.24	-1.41	1.06	-1.22	0.16	-0.69	0.92	-0.06	0.63	CD34 antigen	AA000252		possible adhesion molecule with a role in early hematopoiesis by mediating the attachment of stem cells to the bone marrow extracellular matrix or directly to stromal cells. could act as a scaffold for the attachment of		Cell Surface Protein	
W40995	1.00	1.18	-3.29	1.32	-1.94	0.73	-0.62	0.85	-0.07	0.70		W40995				EST; Unknown	
U19118	1.00	2.01	-0.96	0.81	-0.83	1.97	-1.82	0.18	-0.09	0.66	activating transcription factor 3; Atf3	U19118	cyclic-amp-dependent transcription factor atf-3 (activating transcription factor 3) (transcription factor 1g-21).	this protein binds the camp response element (cre) (consensus: 5'ggacgt(a/c)(a/g)-3'), a sequence present in many viral and cellular promoters. represses transcription from promoters with atf sites. it may repress transcription by stabilizing the binding of inhibitory co-			
Msa.6450.0	1.00	-2.94	-2.22	1.18	-1.31	0.28	-1.43	0.25	-0.13	0.72	early quiescence protein-1; Eql	AA038318					
AA028265	1.00	-2.59	-1.71	1.05	0.65	2.25	-0.62	1.07	-0.13	1.09	fibromodulin	AA028265		fibromodulin, small collagen-binding proteoglycan of the extra-cellular matrix, mainly expressed in articular cartilage, tendon, ligament, leucine-rich repeat (lrr) family believed to function in the assembly of the collagen network in		ECM (Matrix Prot)	

**700**

Accession	1.00	2.11	-0.56	1.01	-0.01	1.28	-0.56	1.01	-0.13	0.74	glucocorticoid-induced leucine zipper; Gilz	AA097366	expressed in normal lymphocytes from thymus, spleen, and lymph nodes, low or no expression detected in other nonlymphoid tissues, including brain, kidney, and liver. selectively protects t cells from apoptosis induced by	Transcription Factor
Msa.15338.0	1.00	1.99	-2.86	2.12	-0.02	1.43	-1.17	1.15	-0.17	0.99	actin alpha 3; Actm3	AA038082	transfected with actin and	
M22326-2	1.00	-1.55	-1.30	0.87	-2.26	0.11	-1.73	0.45	-0.29	0.85	early growth response protein 1 (egr-1) (krox-24 protein) (zif268).	M22326	transcriptional regulator. recognizes and binds to the dna sequence 5'-cgccccgc-3'(egr-site). activates the transcription of target genes whose products are required for mitogenesis and differentiation	Intracellular Protein
AA028499	1.00	1.67	-2.88	0.88	-0.48	1.69	-2.20	0.37	-0.32	1.28	retinol binding protein 4, plasma; Rbp4	AA028499	rbp delivers retinol from the liver stores to the peripheral tissues. in plasma, the rbp- retinol complex interacts with transhyretin, this prevents its loss by filtration through the kidney glomeruli	
Msa.5528.0	1.00	-2.83	-3.31	0.38	-3.53	2.03	-2.06	0.49	-0.44	0.97		W11638		
W35693	1.00	2.57	-1.92	0.93	-0.25	1.56	-0.30	0.98	-0.61	0.56	EST; Unknown	W35693	EST;	
Msa.2579.0	1.00	-2.09	-3.10	1.53	-0.55	1.69	-2.70	0.93	-0.63	0.78	DNA segment, human D4S114;	X70398	expressed in cns	Unknown Other
AA048018	1.00	2.01	-1.54	0.61	0.10	1.39	-0.52	0.89	-0.70	0.69	retinol binding protein 4, plasma	AA048018	plasma retinol binding protein (rbp4) and transhyretin complex with retinol to transport it from storage sites in the liver to target tissues. retinol modulates epithelial morphogenesis and epithelial	Extracellular Protein
Msa.2975.0	1.00	-2.13	-3.13	1.51	-0.57	1.76	-0.61	0.84	-0.71	0.66		W14367		

\*

Accession	1.00	1.85	-0.94	0.71	-0.32	1.40	4.80	1.20	-0.72	0.81	myogenic factor 6; Myf6	X59060	myogenic factor myf-6 (herculin).	myf6 or herculin is expressed in adult skeletal muscle, but not in smooth muscle, cardiac muscle, or non- muscular tissues. it activates expression of myod1 and myog. the level of expression of herculin is higher than for any of the other	10 59.0 cM	Transcriptio n Factor
Msa.15200. 0	1.00	-3.48	-3.48	2.00	-1.38	0.16	-1.75	0.30	-0.72	0.58	CD34 antigen	W65699		possible adhesion molecule with a role in early hematopoiesis by mediating the attachment of stem cells to the bone marrow extracellular matrix or directly to stromal cells. could act as a scaffold for the attachment of		Cell Surface Protein
AA530179	1.00	1.05	-3.59	2.01	-0.08	2.05	-3.74	0.67	-0.74	1.69	S100 calcium binding protein A3; S100a3	AA530179	s100 calcium- binding protein a3 (s-100e protein).	binds both calcium and zinc. probably binds 2 zinc ions per molecule.(by	3 43.6 cM	
Msa.7352.0 AA562685	1.00	1.81 -1.16	-2.64 -2.39	0.53 0.61	-0.82 -0.55	2.09 2.04	-0.65 -0.95	0.85 1.17	-0.76 -0.79	0.70 0.84	procollagen, type I, alpha 1	AA008667 AA562685		type I collagen is of particular importance in the extracellular matrix of bone, skin, tendon, and dentine, and is highly expressed in fibroblasts. it is known to be expressed in mouse palatal shelves		ECM (Matrix Prot)
Msa.723.0	1.00	-2.06	-2.76	1.29	-1.31	0.12	-0.57	0.81	-0.82	0.62	aquaporin 1; Aqp1	L02914	aquaporin-chip (water channel protein for red blood cells and kidney proximal tubule) (aquaporin 1) (early response protein, der2)	forms a water-specific channel that provides the plasma membranes of red cells and kidney proximal tubules with high permeability to water	6 27.0 cM	Cell Surface Protein
Msa.17890. 0	1.00	1.98	-3.38	2.16	-0.23	1.33	-1.21	0.05	-0.86	0.69	eukaryotic translation elongation factor 2; eef2	W98531				

# Table 1: The 200

K02108	1.00	2.14	-0.92	1.29	0.82	1.99	0.19	1.31	-0.86	0.84	keratin complex 2, gene 6a; Krt2-6a	K02108	keratin, type ii cytoskeletal 6 (cyokeratin 6) (ck 6) (k6 keratin).	there are two types of cytoskeletal and microfibrillar keratin: i (acidic; 4-55 kda) [k9 to k2] and ii (neutral to basic; 56-7 kda) [k1 to k8]. both a basic and an acidic keratin are required for filament assembly.	15		
AA185284	1.00	2.23	-2.22	0.43	-0.83	1.88	-1.32	0.14	-0.86	0.64		AA185284					
W41417	1.00	3.44	-2.19	1.11	-0.36	1.43	-1.53	0.23	-0.94	0.83		W41417					
Msa.1170.0	1.00	1.37	-3.82	2.50	0.06	2.16	-2.69	0.44	-0.98	1.39	keratin-associated protein 5-1; Krtap5-1	M37759		keratin-associated protein 5-1		Other	
W81858	1.00	1.23	-2.53	0.85	-0.68	1.89	-1.81	1.47	-1.07	0.94	kinesin light chain 1; Klc1	W81858			12 57.0 cM		
C77823	1.00	1.13	-1.83	0.58	-0.57	2.16	-0.67	1.04	-1.08	0.83		C77823					
AF020194	1.00	1.05	-3.83	2.27	-0.41	1.77	-1.05	1.19	-1.08	0.80	taurine/beta-alanine transporter; Taut	AF020194	sodium- and chloride-dependent taurine and beta-alanine transporter.	an amino acid transporter; found primarily in brain.	6 38.2 cM	Cell Surface Protein	
Msa.43191.0	1.00	1.18	-3.36	0.99	-1.28	2.65	-0.86	1.24	-1.09	0.96	integrin-associated protein; Itgp	Z25524				Cell Surface Protein	
X63023	1.00	2.54	0.34	0.51	0.25	1.30	-1.13	0.04	-1.14	0.03	cytochrome P450, steroid inducible 3a13; Cyp3a13	X63023	cytochrome p450 3a13 (ec 1.14.14.1) (cyp3a13).	can activate aflatoxin b1 to a genotoxic product.	5		
Msa.22263.0	1.00	-2.02	-1.25	1.32	-0.12	1.28	-0.50	0.92	-1.17	0.11		AA033333					
C80656	1.00	1.58	-3.32	1.44	-0.59	1.91	-0.79	2.01	-1.20	0.87	Unknown	C80656				EST;	
Msa.1531.0	1.00	1.97	-2.54	1.23	-1.29	0.24	-0.65	0.88	-1.21	0.07	apolipoprotein D; Apod	L39123	apolipoprotein d precursor.	apod occurs in the macromolecular complex with lecithin-cholesterol acyltransferase. it is probably involved in the transport and binding of bilin. appears to be able to transport a variety of ligands in a number of different contexts.	16 21.2 cM	Unknown Extracellular Protein	
Msa.9372.0	1.00	1.75	-2.72	1.03	-1.67	0.58	-2.02	0.43	-1.22	0.76	CD59 antigen; Cd59	W41339			2 55.0 cM		

# Table 2001

Msa.383.0	1.00	2.36	-1.59	2.09	-0.22	1.48	-1.20	0.07	-1.28	0.12	erythrocyte protein band 4.1; Eppb4.1	L00919	protein 4.1 (band 4.1) (p4.1).	protein 4.1 is a major structural element of the erythrocyte membrane skeleton. it plays a key role in regulating membrane physical properties of mechanical stability and deformability by stabilizing spectrin-actin interaction. binds with a high affinity to glycophorin and with lower affinity to band	4 65.7 cM	Intracellular Protein
X82648	1.00	2.15	-1.74	0.84	-1.17	0.14	-0.69	0.88	-1.32	0.08	apolipoprotein D; Apod	X82648	apolipoprotein d precursor.	apod occurs in the macromolecular complex with lecithin-transport and binding of bilin. appears to be able to transport a variety of ligands in a number of different contexts	16 21.2 cM	Other
Msa.5789.0	1.00	1.98	-3.40	2.07	-0.23	1.46	-0.65	1.07	-1.34	0.16		W18503				
AA673431	1.00	-2.43	-0.84	0.75	0.23	1.52	0.71	1.09	-1.35	0.19		AA673431				EST; Unknown
Msa.5254.0	1.00	-2.55	-2.67	1.27	-1.48	0.08	-1.88	0.35	-1.43	0.13		AA064307				
Msa.21971.0	1.00	1.10	-4.46	1.91	-1.55	2.64	-0.54	1.03	-1.44	0.12		AA154451				
Msa.14179.0	1.00	2.98	-2.90	1.25	-0.15	1.67	-0.92	1.23	-1.47	0.96	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein, 34 kDa), member 17; Slc25a17	AA118682				
AA162560	1.00	1.07	-2.54	0.34	-2.59	0.16	-1.60	0.16	-1.47	0.15		AA162560				
X57024	1.00	1.10	-4.45	2.19	-1.76	0.36	-1.55	0.25	-1.48	0.18	glutamate dehydrogenase; Glud	X57024	glutamate dehydrogenase precursor (ec 1.4.1.3) (gdh).		14 15.5 cM	Metabolic
AA198316	1.00	2.64	-0.11	0.83	1.38	0.08	0.33	1.10	-1.51	0.18	acyl-CoA thioesterase 1, cytosolic; Ctel-1; pending	AA198316			12	



Table "F54E2001"

Msa.2414.0	1.00	1.72	-2.35	1.26	-0.70	0.64	-1.30	0.17	-1.53	0.19	laminin, alpha 3; Lama3	X84014	laminin alpha-3 chain precursor (fragment).	laminin-5 is thought to be involved in (1) cell adhesion via integrin alpha-3/beta-1 in focal adhesion and integrin alpha-6/beta-4 in hemidesmosomes, (2) signal transduction via tyrosine phosphorylation of pp125-fak and p8, (3) differentiation of keratinocytes (by integrin-5).	18.3.0 cM		
AA237919	1.00	-0.03	-2.41	0.90	-0.29	1.68	-1.58	0.35	-1.53	0.46		AA237919					
AA028657	1.00	1.12	-2.28	0.70	-0.54	1.87	-2.01	0.46	-1.60	1.03	EST; Unknown	AA028657				EST; Unknown	
Msa.330.0	1.00	1.53	-5.88	2.92	-2.03	0.91	-1.61	0.39	-1.63	0.36	upstream transcription factor 2; Usf2	U12283	upstream stimulatory factor 2 (upstream transcription factor 2) (major late transcription factor 2).	bhlh protein that is ubiquitously expressed. transcription factor that binds to e-boxes (5'-cacgg-3') found in a variety of viral and cellular promoters. forms bhlh dimers for dna binding. binds dna as homodimer or heterodimer	7.11.0 cM	Transcriptio n Factor	
Msa.40899. 0	1.00	1.40	-2.51	0.86	-1.22	0.17	-3.58	0.96	-1.64	1.30	EST to MYH8	AA162395		m36769 homo sapiens perinatal myosin heavy chain 8% to human			
Msa.42549. 0	1.00	-2.37	-0.31	1.04	-0.14	1.77	-1.06	1.30	-1.65	0.27	est	AA168690		similar to calmodulin		EST; Unknown	
AA266377	1.00	2.21	-1.86	0.25	-1.53	0.40	-1.67	0.31	-1.69	0.22		AA266377					
Msa.8112.0	1.00	-2.17	-2.20	0.84	-0.38	1.57	-0.54	0.89	-1.71	0.97	CD151 antigen; Cd151	AA050218	platelet-endothelial tetraspan antigen 3 (peta-3) (gp27) (membrane glycoprotein sfa-1) (cd151 antigen).		7.23.5 cM		
D17577	1.00	-2.15	-0.33	0.69	1.25	0.06	-1.82	0.43	-1.72	0.24	kinesin heavy chain member 1B; Kif1b	D17577	kinesin-like protein kif1b.	kif1b works as a monomeric motor for anterograde transport of mitochondria.	4.70.9 cM	Structural Protein	

# Table 1

Msa.2160.0	1.00	1.96	-6.25	5.84	-0.10	1.23	-1.32	0.08	-1.72	0.13	apolipoprotein C-I; ApoC1	AA049273	apolipoprotein c-i precursor (apo-ci).	low molecular weight surface component of chylomicrons and of very low density (vldl) and high density (hdl) lipoproteins. functions may include activation of lecithin:cholesterol acyltransferase, and inhibition of apoe binding to the ldl receptor.	7.4.0 cM	Other
U37222	1.00	-2.07	-1.65	0.64	-1.51	0.04	-3.13	1.34	-1.73	0.14	adipocyte complement related protein of 30 kDa; Acrp30	U37222	30 kda adipocyte complement-related protein precursor (acrp30) (adipocyte specific protein adipon)	may function as a signaling molecule for adipose tissue.		
AA237797	1.00	1.15	-2.54	0.76	-0.57	1.88	-2.14	0.54	-1.75	1.03	EST; Unknown	AA237797				EST; Unknown
Msa.33047.0	1.00	-2.09	-1.89	0.98	0.71	0.91	1.19	0.14	-1.76	1.51	CD151 antigen; Cd151	AA109912	platelet-endothelial tetraspan antigen 3 (peta-3) (gp27) (membrane glycoprotein sfa-1) (cd151 antigen).	gene expression was observed in many cell types, but was either absent or present at a low level in brain and lymphoid cells and tissues, including thymus and spleen. contains four putative transmembrane domains, a number of cysteine residues.	7.23.5 cM	Cell Surface Protein
Msa.3770.0	1.00	1.28	-2.88	0.74	-1.69	0.28	-1.62	0.39	-1.79	0.35	peroxisomal membrane protein 3, 35 kDa; Pxm3	L27842	peroxisome assembly factor-1 (paf-1) (peroxin-2).	somehow implicated in the biogenesis of peroxisomes.		
Msa.13629.0	1.00	1.77	-5.94	4.06	-1.56	0.40	-1.67	0.26	-1.80	0.36		AA155371				
Msa.43204.0	1.00	1.11	-1.96	0.42	-1.63	0.42	-2.18	0.61	-1.85	0.83	serine protease inhibitor 1-1; Spl1-1	M75721	alpha-1-antitrypsin 1-1 precursor (serine protease inhibitor 1-1) (alpha- 1 protease inhibitor 1) (alpha-1- 1) (alpha-1- 1)	inhibitor of serine proteases, its primary target is elastase, but it also has a moderate affinity for plasmin and thrombin.	12.51.0 cM	
D30782	1.00	2.46	-0.98	0.66	-1.36	0.17	-2.84	0.63	-1.85	0.18	epiregulin; Ereg	D30782				
W97690	1.00	1.87	-3.28	1.59	-1.46	0.19	-1.78	0.22	-1.97	0.28		W97690				
Msa.40750.0	1.00	1.20	-2.95	0.51	-1.94	0.71	-1.81	0.34	-2.05	0.38	polypyrimidine tract binding protein 2; Ptb2-pending	AA155318				
AF030001E NETNX	1.00	-2.22	-2.62	1.21	-0.40	1.83	-2.62	0.67	-2.06	2.03	Cosmid sequence (>200K)	AF030001				EST; Unknown

Table 3

Z22661	1.00	2.15	-1.65	0.98	-0.43	1.50	-1.72	0.13	-2.11	0.20	apolipoprotein CI; Apoc1	Z22661	apolipoprotein c-i precursor (apo-ci).	appears to modulate the interaction of apoc vldl and inhibit binding of beta-vldl to the ldl receptor-related protein	7.4.0 cM	
Msa.3470.0	1.00	1.04	-1.96	0.78	-1.15	0.14	-3.08	0.53	-2.14	0.38	calsequestrin 1; Casq1	W11481	calsequestrin, skeletal muscle isoform precursor.	calsequestrin is a high-capacity, moderate affinity, calcium-binding protein and thus acts as an internal calcium store in muscle. the release of calcium bound to calsequestrin through a calcium release channel triggers muscle contraction. binds 4 to 5 moles of calcium. also binds		Metabolic
Msa.43184.0	1.00	1.45	-2.47	0.76	-1.34	0.21	-5.16	1.47	-2.20	1.26	myosin, heavy polypeptide 4, skeletal muscle; Myh4	K00988			11.35.0 cM	Structural Protein
M32486	1.00	-1.01	-1.21	0.76	-1.29	0.08	-2.24	0.65	-2.22	0.05	hypothetical protein 19.5; p19.5	M32486		geneseq:nq14534 lov gene (cdna 19.5) - new recombinant polypeptide comprising a t-cell protein - used to regulate t-cell development and tumorigenic phenotype and to block t-cell activation in auto-immune disease. patent held by		Patented; Novel
X90875	1.00	1.47	-3.41	1.29	-2.40	0.52	-2.34	0.43	-2.23	0.14	fragile X mental retardation gene, autosomal homolog; Fxr1h	X90875				
W11010	1.00	2.04	-1.68	0.59	-1.49	0.05	-1.88	0.32	-2.24	0.17	region of homology to: cell division cycle 4-like; beige-like;	W11010				Regulatory

# Table 1: Properties

U30840	1.00	1.36	-1.71	0.55	-1.49	0.32	-1.88	0.17	-2.25	0.09	voltage-dependent anion channel 1; Vdac1	U30840	voltage-dependent anion-selective channel protein 1 (mvdac1) (mvdac5) (outer mitochondrial membrane protein porin 1).	forms a channel through the mitochondrial outer membrane that allows diffusion of small hydrophilic molecules. the channel adopts an open conformation at low or zero membrane potential and a closed conformation at potentials above 3-4 mv. the open state has a weak anion selectivity whereas the closed state is cation-	11 29.0 cM	
J03398	1.00	-1.60	-2.11	0.74	-1.32	0.07	-4.66	0.85	-2.29	1.31	P glycoprotein 2; Pgv2	J03398	multidrug resistance protein 2 (p-glycoprotein 2).	mdr gene encoding a multidrug resistance protein mma	5 1.0 cM	Cell Surface Protein
X61433	1.00	1.06	-1.90	0.33	-1.48	0.10	-2.09	0.36	-2.30	0.12	ATPase, Na+/K+ transporting, beta 1 polypeptide; Atp1b1	X61433	sodium/potassium-transporting atpase beta-1 chain (sodium/potassium-dependent atpase beta-1 subunit).	expressed in brain, kidney, lung, testis, and heart. not found in the liver. expression occurs in pre-b lymphocytes, resting b cells in the bone marrow, pre-t cells, and mature thymocytes. mitogen-stimulated t and b	1 86.8 cM	Cell Surface Protein
Msa.2879.0	1.00	1.32	-2.74	1.40	-1.53	0.12	-2.62	0.14	-2.31	0.27	transducer of ErbB-2.1; Tob1	D78382	tob protein (transducer of erb-2).	anti-proliferative protein that interacts with the erb-2 receptor tyrosine kinase. may physically and/or functionally interact with protein-tyrosine kinase receptors (by stimulation)		

X06115	1.00	1.44	-1.93	0.73	-1.54	0.07	-1.83	0.07	-2.31	0.24	cadherin 1; Cdh1	X06115	epithelial-cadherin precursor (e-cadherin) (uvomorulin) (arc-1).	cadherins are calcium dependent cell adhesion proteins. they preferentially interact with themselves in a homophilic manner in connecting cells; cadherins may thus contribute to the sorting of heterogeneous cell	8 53.3 cM		
Msa.3250.0	1.00	1.14	-4.21	2.32	-1.75	0.48	-1.66	0.34	-2.32	0.40	histidyl RNA synthetase; Hars	U39473	histidyl-tRNA synthetase (ec 6.1.1.21) (histidine--tRNA ligase) (Hars).				
Msa.29324.0	1.00	1.63	-1.48	1.37	-1.32	0.26	-2.00	0.18	-2.33	0.11		AA080197					
Msa.4067.0	1.00	1.73	-2.15	0.61	-0.72	1.74	-0.78	1.03	-2.34	0.57	Sip1?	AA003876		splicing factor (hom sapiens)	Unknown		
Msa.3481.0	1.00	1.28	-2.81	1.61	-1.56	0.02	-2.00	0.09	-2.35	0.13	annexin A8; Anxa8	AA060106			14 13.0 cM	EST;	
AB000713	1.00	-0.50	-1.12	1.24	1.23	0.05	-1.86	0.34	-2.35	0.72	claudin 4; Cldn4	AB000713	claudin-4 (clostridium perfringens enterotoxin receptor) (cpe-receptor) (cpe-r)	a 4 transmembrane domain protein that is a novel component of tight junction strands of liver and kidney.	5 75.0 cM	Unknown Cell Surface Protein	
AA615066	1.00	2.07	-4.34	2.32	-0.57	1.61	-1.58	0.35	-2.38	0.54		AA615066					
Msa.39064.0	1.00	1.13	-2.50	1.11	-1.58	0.22	-2.58	0.28	-2.39	0.18	titin (series elastic element of striated muscle)	AA145312		titin, giant sarcomeric protein, extending from the m line to the z line of striated muscle sarcomere, essential in the temporal and spatial control of the assembly of the highly ordered sarcomeres of striated muscle.		Structural Protein	



Msa.570.0	1.00	1.28	-3.02	2.47	-0.25	1.42	-2.54	0.82	-2.43	0.44	gap junction membrane channel protein beta 2; Gjb2	M81445	gap junction beta-2 protein (connexin 26) (cx26).	one gap junction consists of a cluster of closely packed pairs of transmembrane channels, the connexons, through which materials of low mw diffuse from one cell to a neighboring cell.	14 21.0 cM	
C77662	1.00	1.30	-2.44	0.87	-1.40	0.22	-2.48	0.29	-2.44	0.36		C77662				
Msa.3940.0	1.00	-1.09	-2.21	0.57	-1.72	0.18	-2.20	0.33	-2.44	0.12	Rev-ErbA-alpha protein; rat	W13191		most similar in structure to the thyroid hormone receptor (c-erba) and the retinoic acid receptor, but it does not bind either thyroid hormone or retinoic acid. the mma encoding rev-erba alpha is present in many tissues and is particularly a		Receptor
AA690434	1.00	1.12	-1.86	0.32	-1.84	0.50	-2.52	0.38	-2.45	0.11		AA690434				
M72414	1.00	1.68	-4.09	1.85	-2.21	0.09	-2.62	0.48	-2.47	0.24	microtubule-associated protein 4; Mtap4	M72414	microtubule-associated protein 4;	non-neuronal microtubule-associated protein. promotes microtubule	9 58.0 cM	
Msa.799.0	1.00	-1.57	-3.69	1.19	-2.69	0.73	-2.24	0.25	-2.48	0.30	interferon-related developmental regulator 1; Ifrd1	J00424	interferon-related developmental regulator 1 (nerve growth factor-inducible protein pc4) (tpa induced sequence 7) (tis7 protein).	could play a role in regulating gene activity in the proliferative and/or differentiative pathways induced by ngf. may be an autocrine factor that attenuates or amplifies the initial burst		Cytokine
W29651	1.00	1.11	-4.23	2.14	-1.98	0.01	-2.48	0.34	-2.48	0.30		W29651				
AA688835	1.00	-1.76	-3.43	1.28	-1.97	0.08	-2.48	0.61	-2.51	0.10	Unknown	AA688835			EST;	Unknown
AJ001118	1.00	1.17	-2.97	0.97	-2.10	0.28	-2.89	0.25	-2.56	0.14	monoglyceride lipase; Mgl1	AJ001118			3	
Msa.19265.0	1.00	2.33	-2.61	0.87	-1.88	0.75	-1.96	0.52	-2.57	0.53	golgi autoantigen, golgin subfamily a, 4; Golga4	AA009086				
AF026489	1.00	1.67	-2.26	0.77	-1.75	0.32	-2.22	0.24	-2.62	0.19	beta-spectrin 3; Sptb3	AF026489			19 0.0 cM	
Msa.28719.0	1.00	1.54	-3.87	1.00	-3.39	1.49	-2.22	0.10	-2.65	0.05		AA072611				

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Msa.9757.0	1.00	1.17	-7.61	6.54	-1.66	0.42	-2.17	0.25	-2.67	0.19	basic transcription element binding protein 2; KIF5 desmocollin 1; Dsc1	AA014295	desmocollin 1a/1b precursor.	component of intercellular desmosome junctions. involved in the interaction of plaque proteins and intermediate filaments mediating cell-cell adhesion. may contribute to epidermal cell positioning (stratification) by mediating differential adhesiveness between cells that express different isoforms. linked to the			
X97986	1.00	1.11	-1.97	1.84	-1.42	0.40	-3.01	1.27	-2.71	0.34		X97986					
Msa.32581.0	1.00	1.41	-2.38	1.08	-1.25	0.21	-2.58	0.43	-2.72	0.11	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4; Slc25a4	AA107658	adp,atp carrier protein, heart/skeletal muscle isoform t1 (adp/atp translocase 1) (adenine nucleotide translocator 1)/aat1	carries adenosine triphosphate (atp) from the mitochondrial matrix into the intermembrane space and the diphosphate (ada) in the reverse	8 26.0 cM	Other	
Msa.450.0	1.00	-1.56	-3.38	1.69	-1.73	0.11	-4.22	2.40	-2.74	0.20	adipsin; Adn	W36455	complement factor d precursor (c3 3.4.21.46) (c3 convertase activator) (properdin factor d) (adipsin) (28 kda protein, adipocytin)	a serine protease synthesized principally in adipose tissue, but also by sciatic nerve... adipsin is suppressed (more than 1-fold) in genetically obese mice	10 43.0 cM	Proteolytic	
Msa.111196.0	1.00	1.31	-1.76	0.72	-1.74	0.44	-1.70	0.37	-2.74	0.24		W50088					
U06670	1.00	1.16	-2.84	1.03	-1.65	0.01	-3.54	1.46	-2.75	0.44	very low density lipoprotein receptor; Vldlr	U06670	very low-density lipoprotein receptor precursor (vldl receptor).	binds vldl and transports it into cells by endocytosis. in order to be internalized, the receptor-ligand complexes must first cluster into clathrin-coated pits	19 20.0 cM	Receptor	



Msa.23977.0	1.00	1.39	-2.52	1.29	-1.22	0.04	-2.57	0.68	-2.76	0.26	EST	W07946			geneseq:nz9721 human secreted protein gene 3 cdna clone hwhgu54, seq id no:13. new isolated human genes and the secreted treatment of e.g. cancers			
W71831	1.00	1.37	-5.51	3.22	-1.70	0.18	-3.58	1.40	-2.76	0.36	histone deacetylase 5; Hdac5	W71831						
U12785	1.00	1.04	-2.41	0.64	-1.96	0.28	-2.62	0.39	-2.77	0.07	alcohol dehydrogenase family 3, subfamily A1; Aldh3a1	U12785	aldehyde dehydrogenase, dimeric nadp- preferring (ec 1.2.1.5) (aldh class 3) (dioxin-inducible aldehyde dehydrogenase-3); .fatty aldehyde dehydrogenase (ec 1.2.1.3) (aldehyde dehydrogenase, microsomal) (aldh class 3).	aldhs play a major role in the detoxification of alcohol-derived acetaldehyde. they are involved in the metabolism of corticosteroids, biogenic amines, neurotransmitters, and lipid peroxidation. this protein preferentially oxidizes aromatic aldehyde substrates. it may play a role in the oxidation of toxic	11.34.25			
AA462409	1.00	1.14	-1.61	1.30	-1.49	0.25	-2.23	0.31	-2.81	0.04	Unknown	AA462409					EST;	
Msa.4575.0	1.00	-1.01	-2.05	1.68	-1.47	0.36	-2.53	0.73	-2.81	0.20	EST	AA065868			geneseq:nz56885 human sbpsapl polypeptide encoding est derived sequence. new polypeptides of prosaposin family, antagonist and inhibitors for treatment			Unknown
Msa.16748.0	1.00	2.17	-2.91	1.31	-1.55	0.39	-2.81	0.81	-2.83	0.59		W78443						
Msa.3237.0	1.00	1.01	-2.22	1.69	-1.64	0.57	-1.49	0.07	-2.83	0.29	four and a half LIM domains 1; Fhl1	W14830			fhl1 and fhl3 were expressed in a number of skeletal muscles while fhl2 was expressed at high levels in cardiac muscle. may have an involvement in muscle	X A6-A7.1	Regulatory	

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AA028770	1.00	0.02	-2.96	1.22	-0.34	1.56	-2.74	0.63	-2.86	1.02	Cysteine Rich protein 2, rat	AA028770		expressed in differentiated vascular smooth muscle cells. during development crp2/smlm expression decreased in the heart but remained high in the vasculature.		Regulatory
M91236	1.00	1.28	-2.27	1.21	-1.61	0.53	-2.93	1.20	-2.86	0.27	gap junction membrane channel protein beta 5; Gjb5	M91236	gap junction beta-5 protein (connexin 30.3) (cx30.3).	one gap junction consists of a cluster of closely packed pairs of transmembrane channels, the connexons, through which materials of low mw diffuse from one cell to a neighboring cell.	4 57.5 cM	
W62701	1.00	1.71	-3.09	2.19	-0.68	0.74	-2.36	0.14	-2.88	0.52		W62701				
Msa.6594.0	1.00	1.58	-1.24	1.11	-0.37	1.53	-4.56	2.63	-2.92	0.36		W30612				
Msa.7275.0	1.00	1.19	-1.82	1.28	-1.28	0.03	-2.67	0.32	-2.95	0.31	Mus musculus phosphofructokinase-1 A isozyme (Pfkfb1)	W17917				
Msa.26512.0	1.00	1.31	-1.53	1.17	-1.38	0.29	-2.28	0.39	-3.01	0.48	tubulin alpha 8; Tubaa8	AA063914				
X13135	1.00	1.12	-4.53	1.73	-2.16	0.14	-3.08	0.44	-3.06	0.45	fatty acid synthase; Fasn	X13135	fatty acid synthase (fas) catalyzes the last step in the fatty acid biosynthetic pathway.		11 72.0 cM	Metabolic
Msa.3669.0	1.00	-1.55	-1.69	0.98	-1.64	0.34	-2.26	0.62	-3.06	0.28	est	W08486				EST; Unknown
AA138388	1.00	1.25	-2.10	0.49	-1.90	0.24	-1.97	0.25	-3.07	0.63		AA138388				
U62295	1.00	1.09	-3.22	1.18	-1.83	0.38	-2.99	0.47	-3.07	0.10	cytochrome P450, 2j6; Cyp2j6	U62295	cytochrome p450 2j6 (ec 1.14.14.1) (cyp1j6) (arachidonic acid epooxygenase).		4 46.5 cM	
Msa.2753.0	1.00	-1.18	-5.10	2.45	-1.92	0.61	-2.80	0.31	-3.08	0.53	laminin, beta 2; Lamb2	U43541	laminin beta-2 chain precursor.	extracellular matrix glycoproteins which are major components of basement membranes	9 60.0 cM	ECM (Matrix Prot)
AA734300	1.00	1.09	-2.42	0.84	-1.93	0.62	-2.71	0.59	-3.10	0.48	Hypothetical protein FLJ20171; human	AA734300				Unknown

# Table 2

Msa.717.0	1.00	-1.17	-4.27	2.07	-1.93	0.53	-5.02	1.56	-3.12	0.59	glycerol-3-phosphate dehydrogenase 1, cytoplasmic adult; Gdc1	M13366	glycerol-3-phosphate dehydrogenase [nad+], cytoplasmic (ec 1.1.1.8) (gpd-c) (gndh-c)	belongs to the nad-dependent glycerol-3-phosphate dehydrogenase family.	15 36.8 cM	Metabolic
AA409316	1.00	1.83	-2.55	1.34	-1.53	0.46	-3.69	0.33	-3.12	0.71	Unknown	AA409316				
Msa.12516.0	1.00	1.38	-2.89	1.39	-1.30	0.19	-2.89	0.42	-3.12	0.54	Unknown	W55004			Unknown	
Msa.41264.0	1.00	1.77	-5.60	2.99	-1.66	0.56	-7.59	2.64	-3.17	1.80	myosin heavy chain EST to	AA162315		myh8		Structural Protein
L04678	1.00	1.47	-3.65	1.95	-1.38	0.37	-1.80	0.40	-3.18	0.26	integrin beta 4; Itgb4	L04678			11 76.0 cM	
Z22866	1.00	1.92	-2.24	0.85	-1.62	0.34	-3.33	0.70	-3.19	0.76	myomesin 1; Myom1	Z22866				
Msa.726.0	1.00	1.50	-3.07	1.42	-1.49	0.04	-2.21	0.08	-3.21	0.73	glutathione-S-transferase, alpha 2 (Yc2); Gsta2	W29265	glutathione s-transferase g41a (ec 2.5.1.18) (gst glass-alpha)	liver enzyme;	9 44.0 cM	Metabolic
U31510	1.00	1.18	-4.17	2.06	-2.06	0.23	-1.40	1.32	-3.21	0.39	ADP-ribosyltransferase 1; Art1	U31510	gpi-linked nad(p)(+) -arginine adp-ribosyltransferase precursor (ec 2.4.2.31) (mono(adp-ribosyl)transferase) (yac-1).poly (adp-ribose) polymerase (ec 2.4.2.30) (parp) (adprt) (nad(+) adp-ribosyltransferase) (poly(adp-ribose) synthetase).	poly(adp-ribose) polymerase modifies various nuclear proteins by poly(adp-ribose)ylation. the modification is dependent on dna and is involved in the regulation of various important cellular processes such as differentiation, proliferation, and tumor transformation and also in the regulation of the molecular events involved in the recovery of cell from	7 50.0 cM	Metabolic
Msa.3511.0	1.00	2.20	-1.47	0.57	0.08	1.27	-1.85	0.37	-3.23	0.71	aldolase 3, C isoform; Aldo3	W53351	fructose-bisphosphate aldolase c (ec 4.1.2.13) (brain-type aldolase) (fraement)		11 44.98 cM	
AA691651	1.00	1.12	-2.64	0.65	-1.94	0.58	-2.90	0.47	-3.24	0.30	EST; Unknown	AA691651			EST; Unknown	
X51905	1.00	1.55	-5.30	3.66	-1.51	0.09	-2.88	0.28	-3.28	0.36	lactate dehydrogenase 2, B chain; Ldh2	X51905	l-lactate dehydrogenase h chain (ec 1.1.1.27) (ldh-b)		6 62.0 cM	Metabolic
W15862	1.00	1.30	-1.53	0.84	-1.60	0.30	-3.12	0.84	-3.29	0.40	uncoupling protein 2, mitochondrial; Ucp2	W15862	uncoupling protein 2 (ucp 2) (ucph)	blast of 12/99 = no match	7 50.0 cM	Intracellular Protein

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Msa.30092.0	1.00	1.23	-8.99	6.81	-1.44	0.05	-5.46	1.82	-3.29	0.54	myosin, heavy polypeptide 3, skeletal muscle, embryonic; Mvh3 EST to LTBP4	AA089202	myosin heavy chain, fast skeletal muscle, embryonic (fragment)	muscle contraction.	11 35.0 cM		
Msa.23986.0	1.00	-1.13	-2.92	0.87	-1.80	0.13	-3.03	0.46	-3.30	0.65	EST to LTBP4	W16389	latent transforming growth factor 6% nucleotide level				
AA423082	1.00	1.23	-2.92	0.98	-1.73	0.72	-2.72	0.71	-3.37	0.72	Unknown	AA423082				EST;	
Msa.21797.0	1.00	1.31	-2.77	0.75	-1.85	0.02	-3.30	0.31	-3.44	0.32	ADP-ribosyltransferase 3 (Art3)	AA028701				Unknown	
Msa.1286.0	1.00	1.60	-3.15	1.51	-2.15	0.66	-6.37	2.47	-3.45	1.64	wingless-related MMTV integration site 4; Wnt4	M89797	wnt-4 protein precursor.	may be an intracellular signaling molecule involved in segmentation of the forebrain. is likely to signal over only few cell diameters (by similarity). seems to be involved in kidney development.	4		
X51829	1.00	1.04	-4.58	2.18	-2.40	0.50	-2.90	0.28	-3.48	0.39	myeloid differentiation primary response gene 116; Myd116	X51829	myeloid differentiation primary response protein myd116.			Other	
Msa.3168.0	1.00	1.09	-3.46	1.73	-1.64	0.00	-2.65	0.18	-3.66	0.88	gap junction membrane channel protein beta 6; Gjb6	Z70023	gap junction beta-6 protein (connexin 30) (cx30).	one gap junction consists of a cluster of closely packed pairs of transmembrane channels, the connexons, through which materials of low mw diffuse from one cell to a neighboring cell.	14		
ET62740	1.00	2.18	-2.68	0.86	-2.03	0.73	-2.43	0.60	-3.69	0.95	ankyrin 3, epithelial; Ank3	ET62740			10 38.0 cM		
M74495	1.00	-1.28	-1.86	1.37	-1.22	0.02	-2.60	0.64	-3.70	0.25	adenylosuccinate synthetase 1, muscle; Adss1	M74495	adenylosuccinate synthetase, muscle isozyme (ec 6.3.4.4) (imp-- aspartate ligase) (adss) (amnsase)	plays an important role in the de novo pathway of purine nucleotide biosynthesis.			
AA407234	1.00	1.93	-2.78	0.47	-2.39	1.02	-3.71	1.15	-3.74	0.79		AA407234					

# TABLE 3

U76618	1.00	1.16	-1.51	1.02	-1.52	0.24	-1.60	0.21	-3.77	0.45	rebulin-related anchoring protein; Nrap	U76618		specific to skeletal and cardiac muscle, not detected by northern blot in non-muscle. localized at myotendinous junction in mouse skeletal muscle and intercalated disc in cardiac muscle. plays a role in anchoring a desmin protein.	19 53.25 cM	Structural Protein
AA717225	1.00	-1.07	-2.01	0.52	-1.49	0.03	-2.85	0.77	-3.80	0.63		AA717225		implicated in the control of feeding and in secretion of gonadotrophin-release hormone.		Other
Msa.15880	1.00	-5.84	-2.18	1.33	-1.49	0.24	-2.09	0.30	-3.81	0.73	neuropeptide Y; NPY	W70782		implicated in the control of feeding and in secretion of gonadotrophin-release hormone.		Other
M81086	1.00	1.11	-2.08	0.96	-1.62	0.39	-5.80	3.35	-3.82	0.31	tropomyosin 2, beta; Tpm2	M81086		an actin-associated cytoskeletal protein. different isoforms occur in skeletal muscle and in smooth muscle and nonmuscle cells.		Structural Protein
AF026072	1.00	-0.16	-1.09	1.73	-0.29	1.69	-2.40	1.47	-3.83	1.01	hydroxysteroid sulfotransferase; SULT2B	AF026072				
C80836	1.00	1.45	-3.34	1.10	-2.41	0.17	-6.22	1.90	-3.83	1.08	EST; unknown	C80836				EST; Unknown
AA265119	1.00	-2.16	-2.71	0.67	-2.32	0.55	-6.91	3.49	-3.90	0.53	EST; Unknown	AA265119				EST; Unknown
D42048	1.00	-1.41	-1.83	1.36	-1.80	0.64	-2.87	0.48	-3.92	0.40	squalene epoxidase; Sqle	D42048		catalyzes the first oxygenation step in sterol biosynthesis and is suggested to be one of the rate-limiting enzymes in this pathway.		
Msa.400.0	1.00	1.24	-4.47	1.71	-2.24	0.01	-4.10	0.65	-3.98	0.71	myosin heavy chain, cardiac muscle, adult; Myhca	M76601		adult cardiac specific isoform of myosin heavy chain. (see additional information for regulation).	14 20.0 cM	Structural Protein
U76371	1.00	1.17	-1.64	1.11	-0.08	1.23	-4.77	1.17	-4.01	1.08	CD8beta opposite strand; Bop	U76371		a transcribed gene designated as bop. is a cd8-beta opposite direction transcript. detected in mouse thymus only, and may be limited to cd8+ t cells.	6 30.5 cM	Other

Msa.5248.0	1.00	1.53	-3.03	1.51	-1.52	0.11	-3.41	0.56	-4.02	0.44	phosphofructokinase-1 A isozyme (PfkA)	W11082		defects in pfkm are the cause of glycogen storage disease vii (gsd-vii) (also known as tarui's disease); a disease characterized by exercise intolerance with associated nausea and vomiting		Metabolic
U15541	1.00	1.39	-1.98	1.01	-1.30	0.23	-3.58	1.33	-4.05	0.43	cytochrome c oxidase, subunit VIIIb; Cox8b	U15541	cytochrome c oxidase polypeptide viii-heart precursor (ec 1.9.3.1).	7 68.8 cM	Metabolic	
Msa.1716.0	1.00	1.52	-2.53	1.21	-1.25	0.14	-3.16	0.63	-4.17	0.61	cytochrome c oxidase, subunit VIIIb; Cox8b	AA028501	cytochrome c oxidase polypeptide viii-heart precursor (ec 1.9.3.1).	7 68.8 cM	Metabolic	
Msa.26364.0	1.00	-1.67	-2.77	1.15	-1.53	0.32	-4.00	0.27	-4.18	0.77	mmDNAJA4	AA062328		murine cdna encoding a novel type i hsp4/dnaj homolog. mmджа4(1) biochim. biophys. acta 1493 (1-		Regulatory
Msa.27761.0	1.00	1.08	-6.28	3.32	-2.67	0.08	-2.84	0.35	-4.39	0.45	ethanol induced 6; Etoh16	AA068578				
X61600	1.00	1.16	-2.57	1.60	-1.20	0.04	-11.98	5.36	-4.41	1.00	enolase 3, beta muscle; Eno3	X61600	beta enolase (ec 4.2.1.11) (2-phospho-d-glycerate hydro-lyase) (skeletal muscle enolase)	11 42.0 cM	Metabolic	
AA688542	1.00	1.29	-4.38	2.50	-1.47	0.07	-2.37	0.31	-4.49	0.53	N-myc downstream regulated 2; Ndr2	AA688542	ndrg2 protein (ndr2 protein).			
Msa.2491.0	1.00	-2.38	-6.72	3.49	-2.04	0.41	-3.15	0.11	-4.58	0.59	tenascin X; Tnx	X73959		extracellular matrix glycoproteins probably of importance in regulating developmental processes	17 18.74 cM	ECM (Matrix Prot)
AA033394	1.00	1.52	-3.15	1.22	-1.53	0.19	-5.64	1.78	-4.61	0.82	muscle glycogen phosphorylase; Pygm	AA033394			19 2.0 cM	Metabolic
X67141	1.00	1.04	-3.72	1.84	-0.79	0.74	-7.20	3.32	-4.63	1.28	parvalbumin; Pva	X67141	parvalbumin alpha.	in muscle, the calcium-binding protein parvalbumin is thought to be involved in muscle relaxation.	15 45.7 cM	Extracellular Protein

# Table 200

Msa.6099.0	1.00	1.55	-3.68	1.82	-0.34	1.40	-6.77	1.74	-4.65	1.17	histidine rich calcium binding protein; Hrc	W13030			7 20.4 cM	Regulatory	
AA611262	1.00	1.31	-2.81	0.93	-1.84	0.29	-2.72	0.73	-4.75	0.18	N-myc downstream regulated 2; Ndr2	AA611262	ndrg2 protein (ndr2 protein).	a striated muscle sarcoplasmic reticulum (sr) membrane protein. rapid release and uptake of intracellular calcium is the function of the sr. luminal sr proteins are presumed to function in calcium storage and in			
Y09257	1.00	-1.07	-3.31	1.28	-2.41	0.78	-8.29	2.99	-4.78	0.84	nephroblastoma overexpressed gene; Nov	Y09257	nov protein homolog precursor (novh).	immediate-early protein likely to play a role in cell growth regulation (by similarity).	15 22.5 cM	Signal Transduction	
Msa.728.0	1.00	1.48	-3.39	1.24	-1.69	0.49	-6.12	1.21	-4.91	1.03	solute carrier family 2 (facilitated glucose transporter), member 4; Slc2a4	M23383	glucose transporter type 4, insulin-responsive (gt2).	insulin-responsive glucose carrier protein isoform. glui4. specific to adipose tissue and to skeletal and cardiac muscle.	11 40.0 cM	Cell Surface Protein	
ET61471	1.00	1.77	-5.58	1.40	-5.83	2.05	-3.66	0.36	-4.99	0.57	mast cell protease 7; Mcpt7	ET61471	mast cell protease 7 precursor (ec 3.4.21. ) (nmcp-7) (trypsin).		17 10.4 cM		
Msa.4287.0	1.00	1.32	-3.52	1.57	-1.82	0.09	-6.75	1.84	-5.01	0.68	apolipoprotein B editing complex 2; Apobec2	W29506		apobec-2 mma and protein are expressed exclusively in heart and skeletal muscle. apobec-2 does not display detectable apob mma editing activity. has low, but definite, intrinsic	17 24.0 cM	Intracellular Protein	
M76601	1.00	1.25	-6.73	3.31	-2.47	0.03	-4.62	0.66	-5.31	0.60	myosin heavy chain, cardiac muscle, adult; Myhca	M76601	myosin heavy chain, cardiac muscle alpha isoform.	adult cardiac specific isoform of myosin heavy chain. (see additional information for regulation).	14 20.0 cM	Structural Protein	
X99251	1.00	1.56	-1.54	1.06	-1.59	0.49	-4.38	1.31	-5.36	1.03	repetin; Rptn	X99251	repetin.	novel potential precursor protein of the cornified cell envelope.	3		
Msa.8838.0	1.00	-1.35	-2.43	0.83	-2.79	0.11	-2.90	0.50	-5.40	1.19	myosin light chain, alkali, cardiac ventricles; Mylc	W34697			9 61.0 cM	Structural Protein	

# Protein Data Bank

Msa.13213.0	1.00	1.37	-5.96	3.66	-1.84	0.19	-5.66	0.99	-5.68	0.86	actinin alpha 2; Actn2	W53582	junction plakoglobin (desmoplakin iii) (fragment).	one of the proteins of desmosomal membrane anchorage site plaques of the epithelium, and is also a component of plaques of the adherens junction.	13.7.0 cM	Structural Protein	
Msa.2776.0	1.00	1.32	-3.40	1.87	-1.41	0.24	-2.27	0.48	-6.03	1.83	junction plakoglobin; Jup	M90365	junction plakoglobin (desmoplakin iii) (fragment).	one of the proteins of desmosomal membrane anchorage site plaques of the epithelium, and is also a component of plaques of the adherens junction.	11.60.0 cM	Structural Protein	
AA562768	1.00	2.21	-7.37	1.45	-3.74	2.31	-7.62	2.96	-6.40	1.95	glioblastoma amplified sequence; Gbas	AA562768				Other	
Msa.2946.0	1.00	1.13	-4.57	1.95	-2.15	0.90	-2.87	0.34	-6.70	0.89	cysteine-rich protein 3; Crp3	W08774	ccaa/enhancer binding protein delta (c/ebp delta) (c/ebp-related protein 3); lim domain protein, cardiac (muscle lim protein) (cysteine-rich protein 3)	cardiac lim protein		Transcription Factor	
Msa.727.0	1.00	1.74	-5.46	1.82	-3.53	0.55	-5.48	1.18	-6.92	1.19	glutathione-S-transferase, alpha 3; Gsta3	M73483	glutathione S-transferase yc (ec 2.5.1.18) (gst class-alpha)	conjugation of reduced glutathione to a wide number of exogenous and endogenous hydrophobic electrophiles. this gst has a high catalytic activity for aflatoxin	9.48.0 cM	Metabolic	
Msa.27462.0	1.00	-1.46	-4.50	1.10	-4.40	1.47	-4.02	1.38	-7.09	1.40	growth hormone receptor; Ghr	AA066700	high molecular weight growth hormone receptor/binding protein precursor; low molecular weight growth hormone receptor/binding protein precursor	binding of gh to ghr activates insulin-like growth factor 1 (igf1), which in turn binds to its own receptor to activate signal-transduction pathways leading to growth	15.4.6 cM	Receptor	
Msa.540.0	1.00	1.21	-5.09	2.84	-1.82	0.51	-5.41	1.45	-7.23	1.37	gap junction membrane channel protein beta 4; Gjb4	M91443	gap junction beta-4 protein (connexin 31.1) (cx31.1).	one gap junction consists of a cluster of closely packed pairs of transmembrane channels, the connexons, through which materials of low mw diffuse from one cell to a neighboring cell	4.57.5 cM		



# Protein "Tetrahedron"

Msa.4623.0	1.00	1.37	-6.95	3.61	-1.82	0.25	-8.69	2.10	-7.51	0.45	actinin alpha 2; Actn2	W34429				13 7.0 cM	Structural Protein	
X91825	1.00	1.35	-3.03	1.34	-2.07	0.56	-5.10	0.64	-7.86	1.18	small proline-rich protein 1B; Spr1b	X91825	comifin b (small proline-rich protein 1b) (spr1b) (spr1b)	cross-linked envelope protein of keratinocytes. it is a that first appears in the cell cytosol, but ultimately becomes cross-linked to membrane proteins by transglutaminase. all that results in the formation of an insoluble envelope beneath the plasma	3 45.2 cM			
Msa.17804.0	1.00	-5.76	-4.91	2.21	-1.68	0.14	-4.53	1.89	-8.12	1.86	synuclein, gamma; Snca	AA108571				14 12.5 cM		
Msa.9519.0	1.00	1.22	-10.56	7.86	-1.87	0.70	-10.02	4.21	-8.45	0.47	actinin alpha 2; Actn2	W40754				13 7.0 cM	Structural Protein	
Msa.22711.0	1.00	-1.16	-1.54	1.75	1.07	0.03	-9.74	1.39	-8.51	2.35	creatine kinase, mitochondrial 2 (sarcomeric)	AA038095		reversibly catalyzes the transfer of phosphate between atp and various phosphogens (e.g. creatine phosphate). creatine kinase isoenzymes play a central role in energy transduction in tissues with large, fluctuating energy demands, such as muscle.		Metabolic		
Msa.20143.0	1.00	1.25	-2.76	2.09	-0.75	1.88	-4.08	0.93	-9.86	1.89	hydroxysteroid sulfotransferase; SUL172B	AA016485						
Msa.4317.0	1.00	2.43	-6.26	3.80	-1.72	0.38	-2.62	0.21	-11.22	4.05	calcium channel, voltage-dependent, gamma subunit 1; Cacophony1	AA061886					Cell Surface Protein	
Msa.24682.0	1.00	1.46	-4.33	1.40	-2.98	0.65	-9.23	0.73	-11.22	1.05	ART3 (ADP-ribosyltransferase 3)	W82798		genes: testis specific.			Intracellular Protein	
M88694	1.00	15.59	-3.05	2.20	-0.50	1.50	-6.42	4.80	-11.31	4.10	thioether S-methyltransferase; Temt	M88694	thioether s-methyltransferase (ec 2.1.1.96) (temt).	catalyzes transfer of the methyl group from s-adenosylmethionine to x in compounds of the structure r-x-r', where x may be sulfur, selenium, or tellurium, and r and r' may be various organic substituents.			Other	

# Table 1: Proteins

X79199	1.00	-4.39	-3.08	2.24	-1.82	0.28	-7.10	3.28	-11.54	3.71	tetranectin (plasminogen-binding protein); Tna	X79199	tetranectin precursor (n) (plasminogen- kringle 4 binding protein).	aka plasminogen binding protein -- a plasminogen-binding protein with a c-type lectin domain, is found in both serum and the extracellular matrix. It is a matricellular protein and plays a role in provides a release mechanism for internal cellular $Ca^{2+}$ . mutation associated with human malignant hyperthermia (rhh)(omim 1456). ryr1 is predominant in skeletal muscle, but is also detectable in heart and in brain.	9 71.0 cM	ECM (Matrix Prot)	
X83932	1.00	2.28	-3.02	1.55	-0.27	1.54	-1.90	0.20	-15.56	13.50	ryanodine receptor 1, skeletal muscle; Ryr1	X83932			7 10.0 cM	Receptor	
M91602	1.00	-1.04	-6.76	4.34	-1.48	0.21	-18.83	7.24	-16.81	3.83	myosin light chain, phosphorylatable, cardiac ventricles; MyIpc	M91602	myosin regulatory light chain 2, ventricular/cardiac muscle isoform (mlc-2)	a regulatory light chain predominantly expressed in ventricular cardiac muscle		Structural Protein	
Msa.1007.0	1.00	1.20	-10.87	7.61	-1.90	0.38	-26.29	5.63	-17.28	4.06	myosin light chain, phosphorylatable, cardiac ventricles; MyIpc	M91602	myosin regulatory light chain 2, ventricular/cardiac muscle isoform (mlc-2)	a regulatory light chain predominantly expressed in ventricular cardiac muscle		Structural Protein	
M29793	1.00	1.28	-6.52	3.56	-2.79	0.98	-19.87	14.88	-18.50	9.76	tropoin C, cardiac/slow skeletal; Tncc	M29793	tropoin c, slow skeletal and cardiac muscles (tn-c).	tropoin is the central regulatory protein of striated muscle contraction. tn consists of three components: tn-i which is the inhibitor of actomyosin apase, tn- t which contain the binding site for tropomyosin and tn-c. the binding of tropomyosin	14 10.0 cM	Structural Protein	